

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 148124

TO: Janet Epps-Ford

Location: REM/2C05/2C18

Art Unit: 1635

Friday, March 18, 2005

Search Notes

Case Serial Number: 08/901612

From: David Schreiber

Location: Biotech-Chem Library

Remsen E01A61 Phone: 272-2526

david.schreiber@uspto.gov

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Schreiber, David

From:

Epps-Ford, Janet Thursday, March 10, 2005 4:59 PM Schreiber, David Sent:

To: Subject:

sequence search request

PLease search SEQ ID NOS: 59-65 of application 08/901,612, each sequence is under 30 nucleotides in length. Search all pending and published nucleic acid sequence databases.

Thanks,

Janet L. Epps-Ford, Ph.D.

Art Unit 1635

Mailbox: Remsen 2C18 Office: Remsen 2C05 Phone: 571-272-0757 571-273-0757 Fax:

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

Voluntary Results Feedback Form

| > | I am an examiner in Workgroup: Example: 1610 | | | | | | |
|-------------|---|--|--|--|--|--|--|
| > | Relevant prior art found, search results used as follows: | | | | | | |
| | 102 rejection | | | | | | |
| | 103 rejection | | | | | | |
| | ☐ Cited as being of interest. | | | | | | |
| | Helped examiner better understand the invention. | | | | | | |
| | Helped examiner better understand the state of the art in their technology. | | | | | | |
| | · Types of relevant prior art found: | | | | | | |
| | ☐ Foreign Patent(s) | | | | | | |
| | Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.) | | | | | | |
| > | Relevant prior art not found: | | | | | | |
| | Results verified the lack of relevant prior art (helped determine patentability). | | | | | | |
| | Results were not useful in determining patentability or understanding the invention. | | | | | | |
| Со | Comments: | | | | | | |

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bidg.



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SEARCH REQUEST FORM

Scientific and Technical Information Center

| Requester's Full Name: | | Examiner # : | Date: | |
|---|--|---|----------------------|----------|
| Requester's Full Name: Art Unit: Phoe Mail Box and Bldg/Room Local | ne Number 30 | Serial Number: | | ·, |
| Mail Box and Bldg/Room Loca | ation: F | Results Format Preferred (circle): | PAPER DISK | E-MAIL |
| If more than one search is su | | | | ***** |
| Please provide a detailed statement of Include the elected species or structur utility of the invention. Define any te known. Please attach a copy of the co | es, keywords, synonyms, a erms that may have a specia | cronyms, and registry numbers, and coll meaning. Give examples or relevan | ombine with the con | icept or |
| Title of Invention: | | | | |
| Inventors (please provide full name | | | | |
| • | | | | |
| Earliest Priority Filing Date: | | | | |
| *For Sequence Searches Only* Please is appropriate serial number. | nclude all pertinent informati | ion (parent, child, divisional, or issued pa | itent numbers) along | with the |
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| STAFF USE ONLY D. Sahre ber Gearcher Phone #: 272-2526 | Type of Search | Vendors and cost who | ere applicable | - |
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| earcher Phone #: 272-25 26 | AA Sequence (#) | Dialog | | |
| earcher Location: Remsen Ed / | 96/ Structure (#) | | | <u></u> |
| Date Searcher Picked Up: | Bibliographic | Dr.Link | | |
| rate Completed: 31(8 | Litigation | Loxis/Nexis | | |
| earcher Prep. 1 Review Time: 15 | Fulltext | Sequence Systems Comphy. | ln | . |
| erical Prep Time: | Patent Family | WWW/Internet | | |
| inline Time / O | Other | Other (specify) | | |
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Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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Stuyver, L., Schinazi, R., de Gendt, S., van Geyt, C., Zoulim, F.,
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Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
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Best Local Similarity 86.7%; Pred. No. 0.0036;
Matches 26; Conservative 4; Mismatches 0; Indels
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Oligonucleotides S856459-A 8 05-JAN-1999;
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/organism="unknown"
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Sequence 8 from patent US 5856459.
AR027810
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$67 bp

$60ence 4 from Patent W00138498

AX151115

AX151115.1 GI:14533317
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AF528216
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AF528219
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AF528205 Hepatitis
AF528206 Hepatitis
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M76699 Hepatitis B
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AF528209 Hepatitis
AF528210 Hepatitis
                                                               March 17, 2005, 04:07:57; Search time 1025.6 Seconds (without alignments) 1417.372 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                       4708233 segs, 24227607955 residues
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Maximum Match 100%
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                                              nucleic search, using sw model
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Gaps

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Result õ PAT 22-JUN-2001

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TITLE JOURNAL

FEATURES

ORIGIN

RESULT 3 HPBPRECA/c LOCUS

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REFERENCE AUTHORS

TITLE

gene

CDS

ORIGIN

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FEATURES

COMMENT

ACCESSION VERSION KEYWORDS SOURCE

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HPBPRECC 99 bp DNA linear VRL 11-MAY-1994 Hepatitis B virus type 3precore protein (pre-C region, C) gene, 5'
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/note="g in wt; a in virus type 2 (creates internal stop
codon)"
            Hepatitis B virus type 2precore protein (pre-C region, C) gene,
                                                                                        e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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Hepatitis B virus
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/product="precore protein"
/protein_id="pa445508.1"
/db_xref="GI:485344"
/translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
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Location/Qualifiers
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/mol_type="genomic DNA"
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/organism="Hepatitis B virus"
/mol_type="genomic DNA"
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/note="g in wt; a in virus type 1 (creates internal stop
codon)"
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e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
(bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and Will, H.
Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area virology 183 (2), 840-844 (1991)
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Fried, M. and Rossau, R.
A new genotype of hepatitis b virus
Patent: WO 0138498-A 31-MAY-2001;
Pharmasset, Inc. (US); INNOGENETICS N.V. (BE)
Location/Qualifiers
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100.0%; Score 30; DB 6;
Best Local Similarity 86.7%; Pred. No. 0.0036;
Matches 26; Conservative 4; Mismatches 0;
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linear

DNA

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HPBPRECB

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Gaps

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Gaps

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HPBPRECE 99 bp DNA linear VRL 11-MAY-1994
Hepatitis B virus type 5 precore protein (pre-C region, C) gene, S'
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Hepatitis B virus type 6 precore protein (pre-C region, C) gene, 5'
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95
                                                                                                                                                                                                                                                                                                   e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="AAA45511.1"
db_xref="G1:485350"
/translation="MQLFHLCLIISCSCPTVQPSKLCLGWL"
                                                 Indels
       Query Match
100.0%; Score 30; DB 14; Length
Best Local Similarity 86.7%; Pred. No. 0.0036;
Matches 26; Conservative 4; Mismatches 0; Indels
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10407"
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e antigen; precore protein; tolerogen.
Hepatitis B virus
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/product="precore protein"
                                                                                                        52 GACATGAACAAGAGATGATTAGGCAGAGGT
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Hepatitis B virus type 4 precore protein (pre-C region, C) gene, 5'
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/note="g in wt; a in virus type 3 (creates internal stop
codon)"
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area 91306476
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                                                                                                                                                                            Protein id="AAA45509.1"
/db_xref="GI:485346"
/translation="MQLFHLCLIISCSCPTFQASKLCLGWL"
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                                'note="c in wt; t in virus type 3"
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/mol_type="genomic DNA"
/db_xref="taxon:10407"
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/db_xref="G1:485348"
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/product="precore protein"
'db_xref="taxon:10407"
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M76690.1 GI:485347
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/gene="C"
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/gene="C"
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/qene="C"
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/note="t in wt; c in virus type 6 (loss of start codon)"
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e antique, precore protein; tolerogen.
e antique; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
Hepatitis B virus
Viruses; Retrod viruses; Hepadnaviridae; Orthohepadnavirus.
1 (Dases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
                                                         Will,H.
Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area 91306476
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/standard_name="pre-C region note: putative CDS
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/note="a in wt; g in virus type 7 (gln to arg)"
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'note="putative cds"
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/gene≂"C"
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/gene="C"
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Hepatitis B virus type 8 precore protein (pre-C region, C) gene, 5'
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Hepatitis B virus type 9 precore protein (pre-C region, C) gene, 5'
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/gene="C"
/gene="C"
/gene="g in wt; a in virus type 7 ( creates internal stop
codot)"
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1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and Will, H.
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|standard_name="pre-C region note: putative CDS"
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Location/Qualifiers
                                                                                                                              Query Match 100.0%; Score 30; DB 14; Best Local Similarity 86.7%; Pred. No. 0.0036; Matches 26; Conservative 4; Mismatches 0;
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10. 93
/gene="C"
10. 93
/gene="C"
                                                                                                                                                                                                                                                                                                                                                                                                                                            M76694.
M76694.1 G1:485353
e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
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M76695.1 GI:485354
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Gaps

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PAT 22-JUN-2001

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AF528205 15-JUL-2003 Hepatitis B virus ASC1123 core antigen precursor, gene, partial
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2 (bases 1 to 150)
2 (bases 1 to 150)
3 (andhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
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Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (bases Ito 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stuyver, L., Schinazi, R., de Gendt, S., van Geyt, C., Zoulim, F., Fried, M. and Rossau, R. A new genotype of hepatitis b virus
A new genotype of hepatitis b virus
Patent: WO 0138498-A 3 31-MAY-2001,
Pharmaset, Inc. (US) ; INNOGENETICS N.V. (BE)
Location/Qualifiers
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95
                                                                                                                                                                                                            ; Score 30; DB 14; Length 99;
Pred. No. 0.0036;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                 'standard_name="pre-C region"
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Sequence 3 from Patent WO0138498.
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AX151114.1 GI:14533316
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AF528205.1 GI:32810971
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26; Conservative
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                                                            1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and Will, H.
Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area virology 183 (2), 840-844 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepadnaviridae; Orthohepadnavirus.
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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/note="g in wt; a in virus type 9 (creates internal codon)"
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             Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Location/Qualifiers
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/db_xref="taxon:10407"
10. 99
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antigen; precore protein; tolerogen.
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Hepatitis B virus type 13
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/note="c in w
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/note="g in
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10. .93
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10. .>99
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PUBMED
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Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 150)
Gandhe, S. S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Gandhe, S. S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Submitted (11-UJU-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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/country="India"
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/note="contains partial basal core promoter"
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note="contains complete precore region"
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/organism="Hepatitis B virus"
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                                                                                                              mol type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mol type="genomic DNA"
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AF528206.1 GI:32810973
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Matches 26; Conserva
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AF528206/c
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KEYWORDS
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      Query Match
      100.0%; Score 30; DB 14; Length 150;

      Best Local Similarity 86.7%; Pred. No. 0.0036;

      Matches 26; Conservative 4; Mismatches 0; Indels 0; Gaps

      Qy
      1 GACAUGAACAAGAGAUAGCAGAGGT 30

      Db
      106 GACATGAACAAGAGATTAGGCAGAGGT 77
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Search completed: March 17, 2005, 08:14:15 Job time: 1025.6 secs

us-08-901-612a-59.rng

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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The present sequence represents a synthetic oligonucleotide HBV88b which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "Internucleotide linkages are phosphorothioate"
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                                                                                                                                                                                                                                                                                                                                                                       Hepatitis B virus RNA antisense oligonucleotide HBV88b.
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                                                                                                                                                                                                                                                                ALIGNMENTS
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AAS16092
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AAV82694
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/*tag= a
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 WPI; 1997-043124/04.
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Ad09092 Hepatitis
Aah77563 HBV preCo
Aah77567 HBV genot
Aav82688 Fulminant
Aav82687 Fulminant
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Aad07422 Hepatitis
Aad7122 Hepatitis
Aah77569 HBV genot
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                                                                 March 17, 2005, 04:03:33 ; Search time 257 Seconds (without alignments) 691.020 Million cell updates/sec
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sample. The antisense oligonucleotide, and oligonucleotides containing sequence which is complementary to at least two non-contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
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/*tag= a
/note= "Internucleotide linkages are phosphorothioate"
                                                              Gaps
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                                              ch 100.0%; Score 30; DB 2; Length 30; Similarity 86.7%; Pred. No. 0.003; 26; Conservative 4; Mismatches 0; Indels
                                                                                                                                                             Hepatitis B virus RNA antisense oligonucleotide HBV88Mb.
                                 Sequence 30 BP; 12 A; 3 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                          HBV; HBV infection; inhibition; replication; ss
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/note= "2'-0-methyladenosine"
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                                                                                                                                                                                                                                                                                         note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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                                                                                1 GACAUGAACAAGAGAUGAUUAGGCAGAGGT 30
                                                                                                                                                                                                     Location/Qualifiers
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/note= "2'-OMe RNA"
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The present sequence represents a synthetic oligonucleotide HBV88Mb which is complementary to a portion of the hepatitis B vins (HBV) RM. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non-contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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/*tag= m
/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/note= "2'-0-methyladenosine"
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, Roberts PC, Slade A;
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Roberts NA,
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Fried M;

Zoulim F,

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The present invention relates to hepatitis B virus (HBV) strain FRI, genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreSI, preS2 and surface antigen HBBAG) and HBX proteins. HBV genotype G nucleic acids and polypeptides are useful for diagnosing, prognosing and treating infections caused by HBV genotype G. They can be used in a vaccine to treat or prevent HBV genotype G. They can be used in a vaccine to treat or prevent HBV genotype G infection. The HBV genotype G derived nucleic acids and antibodies are useful for detecting HBV genotype G in a sample or diagnosis of HBV genotype G infection. The presence of HBV genotype G statistically correlates with the presence of liver damage and/or liver cancer in the subject. The HBV genotype G ore insert peptide encoding nucleic acid is useful for designing monitoring assays to study and predict the evolution of anti-HBe and anti-HBC antibodies and HBAAG (genotype G antigen) in patients infected with HBV. The antibodies or antigens of HBV genotype G are useful for identifying a stage of liver disease caused by HBV genotype G DNA fragment encoding e a hepatitis B virus (HBV) strain FRI, genotype G DNA fragment encoding e
                                                                                                                                                                                                                                                                                  Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 30; DB 4; Length 87; Best Local Similarity 86.7%; Pred. No. 0.0035; Matches 26; Conservative 4; Mismatches 0; Indels
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                                                                                                                                                                        Van Geyt C,
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                                                             99US-0167206P.
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                  21-NOV-2000; 2000WO-US032108
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                                                                                                                                                                        Stuyver L, Schinazi R,
                                                                                                    (PHAR-) PHARMASSET INC. (INNO-) INNOGENETICS NV
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                                                             24-NOV-1999;
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                                                                                                                                                                                                                                          screening; antiviral; hepatitis B virus; HBV; DNA polymerase;
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                                                             ADC64742 standard; RNA; 39 BP
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AAD09094 standard; DNA; 87 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-309015/30.
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Matches 26; Conserv
                                                                                                                                                                                                                                                                                                            Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B virus.
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                                                                                                                                                   18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2002.
                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD09094;
                                                                                                         ADC64742;
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Gaps

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protein; preS1; liver disease;

99US-0167206P

24-NOV-1999;

WO200138498-A2

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31-MAY-2001

(PHAR-) PHARMASSET INC

06-OCT-2000; 2000GB-00024544

(CELL-) CELLTECH PHARM LTD

Zoulim F, Fried M;

Van Geyt C,

De Gendt S,

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The present invention relates to hepatitis B virus (HBV) strain FRI, genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreSi, PreSi and surface antigen HBsAg) and HBX proteins. HBV genotype G nucleic acids and polypeptides are useful for diagnosing, prognosing and treating infections caused by HBV genotype G. They can be used in a vaccine to infection cause and antibodies are useful for detecting HBV genotype G derived anucleic acids and antibodies are useful for detecting HBV genotype G in a sample or diagnosis of HBV genotype G infection. The presence of HBV genotype G statistically correlates with the presence of liver damage and/or liver cancer in the subject. The HBV genotype G core insert peptide encoding nucleic acid is useful for designing monitoring assays to study and predict the evolution of anti-HBe and anti-HBc antibodies to study and predict the evolution of anti-HBe and anti-HBV. The and HBAP (genotype G antibodies or antigens) in patients infected with HBV. The attage of liver disease caused by HBV genotype G. The present sequence is a hepatitis B virus (HBV) strain FRI, genotype G DNA fragment
                                                                                                                                                                             Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.
                                                                                                                                                                                                                                                                                     Claim 5; Page 57; 84pp; English.
                                                 Stuyver L, Schinazi R,
(INNO-) INNOGENETICS NV
                                                                                                                              WPI; 2001-367676/38.
                                                                             Rossau R;
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; Score 30; DB 4; Length 129; Pred. No. 0.0038; 4; Mismatches 0; Indels Sequence 129 BP; 25 A; 32 C; 26 G; 46 T; 0 U; 0 Other; Query Match
Best Local Similarity 86.7%; Matches 26; Conservative 4.

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Gaps

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1 GACAUGAACAAGAGAUGAUUAGGCAGAGGT 30 à d

AAD27422 standard; DNA; 639 BP. RESULT 6 AAD27422/

AAD27422;

Hepatitis B virus (HBV) core antigen (HBcAg) encoding DNA #1. (first entry) 18-APR-2002

Hepatitis B virus; HBV; core antigen, HBCAg; immune system; typhoid; prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes; hepatitis C virus; HCV; influenza; foot-and-mouth disease; diarrhoea; tuberculosis; pollo; rables; acquired immunodeficiency syndrome; AIDS; dengue fever; yellow fever; malaria; whooping cough; salmonellosis; food poisoning; meningitis; gonorrhea; antiviral; antibacterial; antiproteozoal; ds.

Hepatitis B virus.

Location/Qualifiers /*tag= a /product= "HBcAq" . 639

WO200198333-A2

27-DEC-2001

22-JUN-2001; 2001WO-GB002817.

22-JUN-2000; 2000GB-00015308

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The invention relates to modified proteins comprising hepatitis B virus (HBV) core antigen (HBCAg) wherein one or more of the four arginine repeats has been deleted and the protein comprising the C-terminal cystaine of HBCAg. The deleted region may be replaced by an epitope from a protein other than HBCAg, in which case the HBCAg acts as a carrier to present the epitope to the immune system. This chimmer protein or its nucleic acid is useful as a vaccine or in a method of prophylactic or therapeutic vaccination of the human or animal body, particularly against HBV. The nucleic acid encoding the protein may be used in gene therapy or DNA vaccination protocols. The chimeric protein or its nucleic acid may also be used as the basis of a prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis A virus (HAV), influenza, foot-and-mouth disease, polio, hepatitis C virus (HCV), influenza, foot-and-mouth disease, polio, hepatitis C virus (HCV), influenza, whooping cough, salmonellosis, vyphoid, food poisoning, diarrhoea, meningitis or gonorrhea. The present sequence is a DNA encoding Hepatitis B virus core antigen (HBCAg)
                                                                                                                                                                                                       vaccine in prophylactic or therapeutic vaccinetion of the human or animal body, particularly against hepatitis B virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                         Disclosure, Page 38-39; 40pp; English.
                                                                                           Li J, Pumpens P;
                                                                                                                                         WPI; 2002-098223/13
                                                                                                                                                                  P-PSDB; AAE17018
                                                                                           Page M,
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Length 639; 0; Indels ch 100.0%; Score 30; DB 6; 1.1 Similarity 86.7%; Pred. No. 0.0049; 26; Conservative 4; Mismatches 0 1 GACAUGAACAAGAGAUGAUUAGGCAGAGGT 30 43 GACATGAACAAGAGATGATTAGGCAGAGGT 14 Query Match Best Local Similarity Matches 26; Conserv ò

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Gaps .; 0

> Hepatitis B virus core antigen (HBcAg) encoding DNA. AAD31509 standard; DNA; 639 (first entry) 18-JUN-2002 AAD31509; RESULT 7 AAD31509/c

Hepatitis B virus core antigen, HBcAg, prophylactic, viral hepatitis, therapeutic, vaccine, acquired immune deficiency syndrome, influenza, polio, herpes, rabies, AIDS, foot-and-mouth disease, ds. 1.87 /*tsg= b /*tag= c /*tag= c /product= "Mature HBc protein" 1, .639 /*tag= a /product= "HBc protein" Location/Qualifiers Hepatitis B virus. sig_peptide mat_peptide

WO200177158-A1

18-OCT-2001

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                                                                                                                                                                                          The present invention relates to hepatitis B virus (HBV) core antigen (HBcAg) fusion proteins and polymucleotides encoding such proteins. Sequences of the invention are useful in methods of prophylactic or therapeutic vaccination or to manufacture medicaments for prophylactic or therapeutic vaccination of the human or animal body against HBV, e.g.
                                                                                                                      vaccines for the
                                                                                                                                                                                                                                                                 The
                                                                                                                                                                                                                                            against viral hepatitis. They are also useful as a prophylactic vaccine against e.g. hepatitis c virus, influenza, pollo, herpes, rables, acquired immune deficiency syndrome (AIDS) or foot-and-mouth disease. The present sequence is a DNA encoding hepatitis B virus core antigen (HBCAG)
                                                                                                                               prophylactic or therapeutic treatment of humans or animals against e.g. HB virus, viral hepatitis, hepatitis C virus, influenza, or foot-and-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tis B virus, HBV; preCore, Core, preS1; preS2, HBS, HBX, HBPol, antiviral, vaccine, genotype G, genotype A, genotyping; HBCAg;
                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                 100.0%; Score 30; DB 6; Length 639; 86.7%; Pred. No. 0.0049;
                                                                                                                                                                                                                                                                                               Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;
                                                                                                                     Hepatitis B (HB) core antigen fusion proteins, useful
                                                                      Rowlands D;
                                                                                                                                                                                                                                                                                                                             Pred. No. 0.00
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                            1 GACAUGAACAAGAGAUGAUUAGGCAGAGGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HBV genotype G strain US1 preCore/Core DNA.
                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                        43 GACATGAACAAGAGATGATTAGGCAGAGGT
                                                                                                                                                                        Disclosure; Page 23-24; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Gendt
                                                                     Stuart D,
                                                                                                                                                                                                                                                                                                                                                                                                                         569/c
AAH77569 standard; DNA; 655 BP.
          09-APR-2001; 2001WO-GB001607
                             07-APR-2000; 2000EP-00107118
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99US-0169287P
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                                                                                                                                                                                                                                                                                                                                        26; Conservative
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                                                 (MEDE-) MEDEVA EURO LTD
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                                                                     Gehin A, Gilbert R,
                                                                                        WPI; 2002-239995/29.
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                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                    P-PSDB; AAE19793
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                                                                                                                                                     mouth disease.
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HBeAg;
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The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G.
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from HBV
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HBCAg;
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genotype A-F molecules, useful for HBV diagnosis, prophylaxis and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBeAg; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30; DB 4; Length 655;
Pred. No. 0.005;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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Best Local Similarity 86.7%; Pred. No. 0.00
Matches 26; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HBV genotype G strain FR2 preCore/Core DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
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                                                            Claim 3; Fig 7; 94pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00870252.
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ID AAH77568 standard; DNA; 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INNO-) INNOGENETICS NV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
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This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBV genotyping. The proteins encoded by the polynucleotides are useful for HBV genotyping. The proteins encoded by the proteins are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins and antibodies directed against HBCAg and HBCAg (precore precursor proteins). They are also useful for preparing a vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/core sequences of an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3, US6, US7, US9, US10) of HBV genotype G \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

4; Length 655; 0; Indels ; Score 30; DB 4; Pred. No. 0.005; 4; Mismatches 1 GACAUGAACAAGAGAUGAUUAGGCAGAGGT 30 100.08; 86.78; 26; Conservative Local Similarity Query Match Matches à

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AAH77574 standard; DNA; 655 BP

(first entry) 19-OCT-2001 AAH77574;

HBV genotype G strain US10 preCore/Core DNA.

Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBV1; HBPol; Antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg; HBeAg; ds.

Hepatitis B virus.

WO200140279-A2

07-JUN-2001.

0-NOV-2000; 2000WO-EP011526

99EP-00870252 99US-0169287P 03-DEC-1999; 07-DEC-1999;

(INNO-) INNOGENETICS NV.

ŝ Gendt De Stuyver L, Van Geyt C,

WPI; 2001-374785/39.

Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and therapy

Claim 3; Fig 7; 94pp; English.

human hepatitis B virus (HEV) genotype, provisionally named genotype of This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Burope and the USA. The invention relates to a fully defined sequence of 3348 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or polynucleotides are useful for HBV genotyping. The proteins encoded by the polynucleotides are useful for HBV genotyping. The proteins a biological The invention relates to the complete nucleic acid sequence of a new AAH17574/C

ID AAH77574/C

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AC AAH7757

XX

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AC AAH7757

DE HBV Gel

XX

HBRAG;

XX

Claim

XX

CC

HBRAG;

present sequence is provided in an alignment of preCore/Core sequences of an HBV genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3, US6, US7, US9, US10) of HBV genotype G sample. Ligands that bind to the proteins and antibodies directed against the proteins are to useful for detecting the proteins and for detecting HBGAg and HBGAg (precore precursor proteins). They are also useful for preparing a vaccine or medicament for treating HBV infections. The 8888888888

Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

Gaps ; 0 4; Length 655; 0; Indels Score 30; DB 4; Pred. No. 0.005; 4; Mismatches Pred. No. 100.0%; 86.7%; F Local Similarity 86.7 tes 26, Conservative Query Match Best Loca Matches

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AAH77573 standard; DNA; 655 BP AAH77573/c RESULT 11

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Gaps

0;

AAH77573;

(first entry) 19-OCT-2001 HBV genotype G strain US7 preCore/Core DNA.

Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol; HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg; HBeAg; ds.

Hepatitis B virus.

WO200140279-A2

07-JUN-2001.

20-NOV-2000; 2000WO-EP011526.

99EP-00870252. 99US-0169287P.

03-DEC-1999; 07-DEC-1999;

(INNO-) INNOGENETICS NV.

De Gendt Stuyver L, Van Geyt C,

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WPI; 2001-374785/39

Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and therapy

Claim 3; Fig 7; 94pp; English.

The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBV genotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies directed against the proteins are useful for detecting antibodies directed against the proteins are useful for detecting the proteins and for detecting the proteins and for detecting the proteins and for medicament for treating HBV are also useful for preparing a vectime or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/Core sequences of an HBV genotype A strain (HBVXCRS) and 7 strains (FRI, FRZ, USI, US3, US1, US3, USG, US7, US9, USIO) of HBV genotype G

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The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the UGA. The invention relates to a fully defined sequence of 3248 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or specification, a degenerate to the Part of the proteins encoded by the polynucleotides are useful for HBV genotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies in a biological cample. Ligands that bind to the proteins and antibodies directed against the proteins are useful for detecting the proteins and excise or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/Core sequences of an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FR2, USI, US3,
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                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus; HBV; preCore; Core; preSl; preS2; HBS; HBY; HBPOl;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
                                                                      Gaps
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                                    DB 4; Length 655;
Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;
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                                                                      0; Indels
                                ; Score 30; DB 4;
Pred. No. 0.005;
4; Mismatches
                                                                                                        1 GACAUGAACAAGAGAUGAUUAGGCAGAGGT 30
                                                                                                                             43 GACATGAACAAGAGATGATTAGGCAGAGGT 14
                                                                                                                                                                                                                                                                                                                                                HBV genotype G strain US3 preCore/Core DNA
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                                    100.08;
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                        Query Match
Best Local Similarity 86.7%;
Marches 26; Conservative
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                                                                                                                                                                                                                                   AAH77570 standard; DNA; 655
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07-DEC-1999;
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The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Burope and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBV genotyping. The proteins encoded by the protucine are useful for detecting and antibodies in a biological sample. Ligands that bind to the proteins and antibodies in a biological the proteins are useful for detecting the proteins and for detecting HBCAS and HBCAS and HBCAS and HBCAS useful for medicament for treating HBV infections. The present sequence is provided in an alignment of precore/core sequences of an HBV genotype. A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3, united the proteins are useful for an HBV genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                                                                                         HBcAg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                       Hepatitis B virus; HBV; preCore; Core; preSl; preS2; HBS; HBX; HBSAg; antivixal; vaccine; genotype G; genotype A; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 655 BP; 138 A; 154 C; 140 G; 195 T; 0 U; 28 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 4; Length 655;
Pred. No. 0.005;
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30
                                                                                                                                                                                                                         HBV genotype G strain US5 preCore/Core DNA.
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4; Mismatches
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                GACATGAACAAGAGATGATTAGGCAGAGGT
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1 GACAUGAACAAGAGAUGAUUAGGCAGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Gendt S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 7; 94pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2000; 2000WO-EP011526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99EP-00870252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0169287P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.78;
                                                                                                                  AAH77571 standard; DNA; 655
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 86.7
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Geyt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-374785/39.
                                                                                                                                                                                                                                                                                                                             Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                               WO200140279-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37-DEC-1999;
                                                                                                                                                                                      19-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stuyver L,
                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2001
                                                                                                                                                                                                                                                                                             da.
                                                                                                                                                    AAH77571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy
                                                                                  RESULT 13
                                                                                                    AAH77571,
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AAH77572/c RESULT 14

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Gaps ö

Query Match 100.0%; Score 30; DB 4; Length 655; Best Local Similarity 86.7%; Pred. No. 0.005; Matches 26; Conservative 4; Mismatches 0; Indels

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HBcAg; immunomodulator; vaccine; gene; ss.

Hepatitis B virus.

/note= "No start codon"

WO2004035007-A2 29-APR-2004

/partial

17-OCT-2003; 2003WO-US033178. 17-OCT-2002; 2002US-0419279P

Location/Qualifiers 10. .669 /*tag= a /product= "HBcAg"

Key

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Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPOl;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
                                                                                                                                                                                                                                   from HBV
                                                                                                                                                                                                                       Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 664 BP; 146 A; 160 C; 144 G; 208 T; 0 U; 6 Other;
                  ί
                                              HBV genotype G strain US6 preCore/Core DNA
                                                                                                                                                                                             De Gendt S;
                                                                                                                                                                                                                                                                Claim 3; Fig 7; 94pp; English
                                                                                                                                       20-NOV-2000; 2000WO-EP011526
                                                                                                                                                       99EP-00870252
                                                                                                                                                              99US-0169287P
AAH77572 standard; DNA; 664
                              (first entry)
                                                                                                                                                                                           Stuyver L, Van Geyt C,
                                                                                                                                                                           (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                          WPI; 2001-374785/39.
                                                                                          Hepatitis B virus.
                                                                                                          WO200140279-A2
                                                                                                                                                      03-DEC-1999;
07-DEC-1999;
                              19-OCT-2001
                                                                                                                        07-JUN-2001
                AAH77572;
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Modulating a systemic immune response to a peptide in a mammal comprises transmucosally administering a macromolecular aggregate of the peptide.

2004-348329/32.

WPI; 2004-348329, P-PSDB; ADO07221

ORAG-) ORAGEN CORP

Michaels F;

Disclosure; SEQ ID NO 1; 81pp; English.

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The present sequence is the DNA sequence of the hepatitis B virus core antigen (HBCAg) gene from HBV serotype ayw. A peptide comprising a HBV protein can be used in claimed methods of the invention for modulating an immune response in a mammal. A method of inducing a systemic immune response to a peptide in a mammal comprises transmucosally administering cresponse to a peptide in a mammal comprises transmucosally administering conformal a macromolecular aggregate of the peptide. The macromolecular weight of over 1,000 kDa, and is preferably at least 5 nm in aggregate form by chemical treatment and/or by recombinant protein aggregate form by chemical treatment and/or by recombinant protein cagineering of the peptide. The peptide preferably comprises a HBV cortein selected from HBV surface protein, nucleocapsid protein or envelope protein. Transmucosal administration to a mammal or esponse in the mammal. A method of suppressing an immune response in the mammal. A method of suppressing an immune response in the mammal. A method of suppressing an immune response in the mammal. A method of suppressing an immune response in the mammal. A method of suppressing an immune response of that is resistant to digestive degradation and which may be stabilised by chemical treatment or protein engineering, and which may be derived from a HBV protein. A monomolecular peptide is useful for the induction of cral tolerance when inductions.

In cases of chronic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 669 BP; 155 A; 170 C; 148 G; 196 T; 0 U; 0 Other;
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Gaps

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0; Indels

100.0%; Score 30; DB 4; Length 664; 86.7%; Pred. No. 0.005;

Pred. No. 0.00 4; Mismatches

Local Similarity 86.7%; les 26; Conservative

Query Match

Best Loc Matches

1 GACAUGAACAAGAGAUGAUUAGGCAGAGGT 30 43 GACATGAACAAGAGATGATTAGGCAGAGGT

Hepatitis B virus core antigen DNA.

15-JUL-2004 (first entry)

AD007220;

RESULT 15
ADO07220/c
ID ADO07
XX
AC ADO07
XX
DT 15-JU
XX
DE HEPAT

7220/c ADO07220 standard; DNA; 669

Hepatitis Hepatitis

Hepatitis Hepatitis

Hepatitis

Hepatitis Hepatitis Hepatitis Hepatitis

Hepatitis

Hepatitis

Minimum DB Maximum DB

Database

Result No.

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Searched:

Hepatitis

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Run on:

Sequence:

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Hepatitis
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Unknown.
Unclassified.
1 (bases 1 to 30)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 30)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
Mills, J.S.
               AF528213
AF528213
AF528214
AF528216
AF528217
AF528219
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                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                              Oligonuclectides specific for hepatitis
Patent: US 5856459-A 8 05-JAN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                      1. .30
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 bp
Sequence 39 from patent US 5856459.
AR027841
                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                     30 bp
Sequence 8 from patent US 5856459.
AR027810.1 GI:5938630
                                              AF528216
AF528217
AF528218
AF528219
AF528220
AF528221
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AF528228
AF528229
AF528231
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AF528234
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AF528236
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Unknown.
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DEFINITION
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AR027810
LOCUS
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SOURCE
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                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
FEATURES
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AUTHORS
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AR027841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX151114 Sequence
AF528205 Hepatitis
AF528207 Hepatitis
AF528207 Hepatitis
AF528209 Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AXIIIIIS Sequence
N76687 Hepatitis B
M76689 Hepatitis B
M76690 Hepatitis B
M76691 Hepatitis B
M76692 Hepatitis B
M76693 Hepatitis B
M76695 Hepatitis B
M76699 Hepatitis B
                                                       March 17, 2005, 04:07:57; Search time 683.733 Seconds (without alignments) 1417.372 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                               AR027810 Sequence
AR027841 Sequence
                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                9416466
       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                4708233 segs, 24227607955 residues
                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AXI51115
HPBPRECA
HPBPRECB
AXI51114
AXI51114
AXI51114
AXI528205
AF528205
AF528207
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AR027841
                                                                                                         gacatgaacaagagatgatt 20
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Gapop 10.0 , Gapext 1.0
                                                                                       US-08-901-612A-60
                                                                                                                                                                               seq length: 0
seq length: 200000000
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gb_sy: *
gb_un: *
gb_vi: *
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gb_ov::,
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Perfect score:
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source

ORIGIN

FEATURES

TITLE JOURNAL

DEFINITION ACCESSION VERSION

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS

RESULT 3 AX151115/c

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HPBPRECB 99 bp DNA linear VRL 11-MAY-1994
Hepatitis B virus type 2precore protein (pre-C region, C) gene, 5'
                                                                                                                                                                                                                                                                                 /gene="C"
/note="g in wt, a in virus type 1 (creates internal stop
codon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="C"
/note="g in wt; a in virus type 2 (creates internal stop
codon)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                            translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="precore protein"
protein_id="AAA45508.1"
db_xref="G1:485344"
/translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source text: Hepatitis B virus DNA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="c in wt; t in virus type 2"
                                                                                                                 /gene="C"
/standard_name="pre-C region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Hepatitis B virus"
mol_type="genomic DNA"
db_xref="taxon:10407"
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                                                                                                                                                                          /product="precore protein"
/protein_id="AAA45507.1"
/db_xref="GI:485342"
              /mol_type="genomic_DNA"
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10._.93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACATGAACAAGAGATGATT 20
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                                                                                                                                                             codon start=1
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M76688.1 GI:485343
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/gene="C"
10. .93
/gene="C"
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KEYWORDS
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HPBPRECB/c
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1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                                                                                                                      Gaps
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A new genotype of hepatitis b virus
Patent: WO 0138498-A 4 31-MAY-2001;
Pharmasset, Inc. (US) ; INNOGENETICS N.V. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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                                                                                                                                                                                           Length 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                    0; Indels
Mills,J.S.
Oligomucleotides specific for hepatitis B virus
Patent: US 5856459-A 39 05-JAN-1999;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 0;
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/organia="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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synthetic construct
other sequences; artificial sequences.
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Hepatitis B virus
Hepatitis B virus

    .99
    /organism="Hepatitis B virus"

                                                                                     1. .30
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4 from Patent W00138498.
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HPBPRECE 11-MAY-1994
Hepatitis B virus type 5 precore protein (pre-C region, C) gene, 5'
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e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
Viruses; Lto 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and Will, H.
Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area
Virology 183 (2), 840-844 (1991)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and Will, H.
                       Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/db_xref="GI:485348"
/translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
                                                                                                                         source text: Hepatitis B virus DNA.
Location/Qualifiers
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                                                                                                                                                                              /organism="Hepatitis B virus"
/mol_type="genomic DNA"
/db_xref="taxon:10407"
10..93
/gene="C"
10..93
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/organism="Hepatitis B virus"
/mol_type="genomic DNA"
/db xref="taxon:10407"
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/standard_name="pre-C region"
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/product="precore protein"
/protein_id="AAA45511.1"
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10. .93
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Hepatitis B virus type 4 precore protein (pre-C region, C) gene, 5'
                                                                                                                                                  HPBPRECC 99 bp DNA linear VRL 11-MAY-1994
Hepatitis B virus type 3precore protein (pre-C region, C) gene, 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="C"
/note="g in wt; a in virus type 3 (creates internal stop
codon)"
                                                                                                                                                                                                                                                                                                                         Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
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/note="g in wt, t in virus type 3 (val to phe)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name="pre-C region"
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/db_xref="GI:485346"
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Location/Qualifiers
1. .99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="c in wt; t in virus type 3"
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/mol_type="genomic DNA"
/db_xref="taxon:10407"
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                           GACATGAACAAGAGATGATT 20
                                             52 GACATGAACAAGAGATGATT 33
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/gene="C"
10. .93
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M76689.1 GI:485345
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HPBPRECC/c
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HPBPRECH 99 bp DNA linear VRL 11-MAY-1994 Hepatitis B virus type 8 precore protein (pre-C region, C) gene, 5'
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hote="g in wt; a in virus type 7 ( creates internal stop
codon)"
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     e antigen, precore protein, tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (Dases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and Will, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                     Prevalence and type of pre-C HBV mutants in anti-HBe positive carriters with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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'standard_name="pre-C region note: putative CDS"
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100.0%; Score 20; DB 14; Length 99;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels
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1..90
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/db_xref="taxon:10407"
10..93
/gene="C"
10..93
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/db_xref="taxon:10407"
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/gene="C"
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                                                                                /gene="C"
/note="g in wt; a in virus type 5 (creates internal stop codon)"
95
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/note="t in wt; c in virus type 6 (loss of start codon)"
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1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area 91306476
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                 translation="MQLFHLCLIISCSCPTVQPSKLCLGWL"
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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:10407"
10._.99
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Hepatitis B virus
Hepatitis B virus
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10...99
/groduct="Precore protein"
/note="putative cds"
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db_xref="GI:485350"
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/gene≂"C"
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HPBPRECM 99 bp DNA linear VRL 11-MAY-1994
Hepatitis B virus type 13 precore protein (pre-C region, C) gene,
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                                                                                                                            e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santanconio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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/note="g in wt; a in virus type 13 (gly to asp)"
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Location/Qualifiers
1. .99
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Patent: WO 0138498-A 3 31-MAY-2001;
Pharmasset, Inc. (US); INNOGENETICS N.V.
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xrefe"taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Hepatitis B virus"
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|10..99
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Sequence 3 from Patent WO0138498.
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synthetic construct
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10. .>99
/gene="C"
                                                                                                                   M76699.1 GI:485361
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Hepatitis B virus type 9 precore protein (pre-C region, C) gene, 5'
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/note="g in wt, a in virus type 9 (creates internal stop
codon)"
                                                                                 /gene="C"
/note="g in wt; a in virus type 8 (creates internal stop
codon)"
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                                                                  8 (loss of start codon)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and Will, H.
Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area virology 183 (2), 840-844 (1991)
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10. .93
//gene="C"
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/standard_name="pre-C region note: putative CDS"
/product="precore protein"
/standard_name="pre-C region note: putative CDS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
/note="g in wt; a in virus type 9 (gly to asp)"
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Location/Qualifiers
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/organism="Hepatitis B virus"
/mol_type="genomic DNA"
/db_xref="taxon:10407"
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/note="g in v
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
I (bases 1 to 150)
Comparative evaluation of HBV precore and basal core promoter
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
Dipublished
E 2 (bases 1 to 150)
E 3 (bases 1 to 150)
S Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
L Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Irce
I.150/Qualifiers
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                                                                                                                                                                                                                                            AF528205 150 bp DNA linear VRL 31-JUL-2003
Hepatitis B virus ASC1123 core antigen precursor, gene, partial
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/db Aref="twanon:10407"
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/country="India"
/lote="contains partial basal core promoter"
/note="contains complete precore region"
/note="contains complete precore region"
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100.0%; Score 20; DB 14; Length 150;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels
Query Match 100.0%; Score 20; DB 6; Length 129; Best Local Similarity 100.0%; Pred. No. 49; Matches 20; Conservative 0; Mismatches 0; Indels
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/isolate="ASC1123"
                                                                                     1 GACATGAACAAGAGATGATT 20
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AF528205.1 GI:32810971
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Search completed: March 17, 2005, 08:14:16 Job time : 684.733 secs

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CD304890 SrPuces

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CG559916 RPC1-23-3

CG559916 BFLG3-001

CW000359 ZMWBLa001

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CD266187 StrPuces

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BG104640 602311331

CG63302 CO2015013

CG63302 STR14-413M

AQ27786 hbxb0028N

CA044022 BBADDAB50

AQ509958 hbxb00094H

AQ509958 hbxb00094H

AQ509958 cCT138440 OR BBAD094

CCT138440 OR BBAD094
                                                                                                     March 17, 2005, 05:44:58; Search time 2079.4 Seconds (without alignments) 549.162 Million cell updates/sec
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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| CA061593 sealrga50 CE72248 tigr-gas- CL779656 OR Baa009 AV070321 AV707321 CA34858 679903 NC CB512505 sealrgb55 CL797320 OR Baa010 CL797320 OR Baa010 CL797320 OR Baa010 CL795294 OR CBa000 CA27122 EST013007 BZ798022 PUGDA69TD BZ64258 OGAMK61TC CD339264 StrPu557 AA003912 mg79e03.r CD330465 StrPu557 AA003912 mg79e03.r CD310469 StrPu691. CB7655 F. rubripes CD310469 StrPu691. CL557140 OB_Ba000 | CG452180 G61 bp DNA linear GSS 17-SEP-2003 G65DV84TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0841N24, CG452180. CG452180. CG452180. GG452180. | " StEB" 5-KB" genomic 1: HincII; 0.7-1.5 kb genomic DNA library" 7: DB 9; Length 661; 1.6e+02; Indels 0; Gaps 0; KT 30 KT 30 KT 452 |
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| CAO61593 CE792348 CE779656 CL612489 AV707321 CA348548 CB512505 CL7933261 AQ687676 CL795294 CL795294 CL795294 CL795294 CL795294 CL795294 CL795294 CL795294 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL7952964 CL795296930 CL7957140 | CG452180 CG5DV84TC ZM 0.7_1.5_KB Zea mays GG452180 CG452180. GG452180. GG452180.1 GI:34837180 GSS. Zea mays Zea mays Zea mays Enaryota; Viridiplantae; Strepto Spermatophyta; Magnollophyta; Lil clade; Panicoideae; Andropogoneae 1 (bases 1 to 661) Whitelaw, C.A., Quackenbush, J., Va Renick, A., Numberg, A., Robbins, D Consortium for Maize Genomics Unpublished (2002) Contact: Cathy Whitelaw 712 Medical Center Drive, Rockvi Tel: 301-838-5843 Fax: 301-838-5843 Fax: 301-838-5863 Class: sheared ends. Location/Qualifiers Location/Qualifiers 1 ocanion-BBT Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location-BBT Anoleype="genomic DNA" Apragn="genomic DNA" Apragn="genomic DNA" | EMa0841N24 "ZM 0.7 1. "ZM 0.7 1. or: pBCSK- filtered Score 22 Pred. No 2; Misma UUAGGCAGAG |
| 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 11.5 937 937 937 937 15 15 15 16 16 17 16 17 19 19 19 19 19 19 19 19 19 19 | ZMM ibb= ion ion 13*; 7*; 7*; |
| 663 698 698 698 707 733 733 734 744 744 744 754 754 754 754 754 754 75 | CG452180 CG5DV84TC ZM_0.7_1.5_KB Z genomic survey sequence. CG452180.1 GI:34837180 CG5SS. Zea mays Zea mays Eukaryota; Viridiplantae; Spermatophyta; Magnolloph clade; Penicoideae; Andro 1 (bases 1 to 661) Whitelaw, C.A., Quackenbus Resnical to 661) Whitelaw, C.A., Quackenbus Resnical to 661) Consortium for Maize Geno Unpublished (2002) Consortium for Maize Geno Unpublished (2002) Fax: 301-838-5843 Fax: 301-838-5643 Fax: 301-838-508 Email: whitelawerighticles Tel: 301-838-508 Email: whitelawerighticles Class: sheared ends. Location/Qualifi 1 cation/Qualifi Arganism="Zea m" / Molation of type="genom" / Arganism="Zea m" / Arganism="Z | /clone="ZMM" /clone lib= /clone lib= /note="Vect" /note=" |
| | of the control of the | Trit mase GAP GAP |
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| 000000000000000000000000000000000000000 | CG452180 CG5DV84TC ZM GG5DV84Z180 CG452180.1 GG5S.1 GGS. Zea mays Zea mays Zea mays Semaryota; Vi Spendrophyta Spendrophyta Spendrophyta Clade; Panico 1 (bases 1 t Whitelaw, C.A. Whitelaw, C.A. Renick, R.W., N Consortium fo Consortium fo Consortium fo Consortium fo Consortium fo Tek, R.W., N TigR Semail: Whitela Fax: 301-838 | /c] /nc//nc//nc//nc//nc//nc//nc//nc//nc//nc |
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 2 CD304890

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 701)
3 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other Soss: RECI-23-370H16.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
Plate: 370 row: H column: 16
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/db_xref="RPCI-23-370H16"
/sex="RPGale"
/lab_host="Emaile"
/lab_host="DH10B"
/lobe="Grgan: Kidney/Brain; Vector: pBAC63.6; Site_1:
RCORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBAC63.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Zea.
       musculus genomic clone
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                                RPCI-23-370H16, genomic survey sequence
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llarity 73.3%; Pred. No. 1.7e+02;
Conservative 3; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
RPCI-23-370H16.TV RPCI-23 Mus
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Mus musculus
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CG359992
CG359992.1 GI:34277259
                                                                                                    AQ993161.1 GI:7068258
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CG359992
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/mol_type="mRNA"
/db_tref="unatus" | /db_tre
                                                                                                                                                                                                                                                                                                                                              SM Strongylocentrocus purpuratus

Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

Echinoidea; Bucchinoidea; Echinocea; Echinoida;

Erinoidea; Bucchinoidea; Echinocea; Echinoida;

Erinoidea; Euchinoidea; Etrongylocentrotus.

E (bases 1 to 643)

Poustka, A.J.; Groth, D.; Hennig, S.; Thamm, S.; Cameron, A.; Beck, A.;

Reinhardt, R.; Herwig, R.; Panopoulou, G. and Lehrach, H.

Generation, amnotation, evolutionary analysis, and database
integration of 20,000 unique sea urchin EST clusters

Contact: Poustka AJ

laboraty 145, dept.lehrach

Max-Planck-Institut fuer Molekulare Genetik

Minnestri 63-73, D-14195 Berlin, Germany
                                                                                  CD304890 663 bp mRNA linear EST 16-SEP-2003 StrPu691,001255 Sea urchin larva CDNA library MPMGp691
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BACKWARD: 5' GCTATTACGCCAGCTGGCGAAGGGGGATGTG 3' (M13FSP)
BACKWARD: 5' GCGGTCCGGAATTCCCGGGT-3' pSport3/86
High quality sequence stop: 663.
Location/Qualifiers
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76.7%; Pred. No. 1.68+02;
Mismatches 5; Indels
                                                                                                                                               Strongylocentrotus purpuratus cDNA clone
MPMGp691C0520,MPI_SURUDI_20C5 5', mRNA sequence.
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Best Local Similarity
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source

FEATURES

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Gaps ö

GSS 24-FEB-2000

linear

DNA

701 bp

A0993161

AQ993161/c LOCUS

RESULT

g

Matches

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/tissue_type="immature ears"
/lab_host="DH10B_T1 phage resistant"
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Plate: 0012 row: A column: 22
Class: BAC ends.
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/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AUGAACAAGAGAUGAUUAGGCAGAGG 29
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/clone="ZMMBLa0012A22"
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1. .843
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The library was characterised by oligonucleotide fingerprinting
(NPF) to reduce sequencing redundancy. According to the ONFP
procedure, clones giving the same hybridisation pattern with a
battery of 200 Bmer oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
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BFLG3_001884 Amphioxus 5-6 hrs cDNa library (Name convention: BFLG or MPMGp498) Branchiostoma floridae cDNa clone MPMGp49800628 5',
           Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGICX42TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Branchiostoma floridae
Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
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New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.3%; Score 22; DB 9; Length 888; 76.7%; Pred. No. 1.78+02; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Panopoulou G
laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
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                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/etrain="B73"
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/clone="ZMMBMa0733H12"
                                                                                                                                                                                                                                                                                                                                                            /organism="Zea mays"
/mol_type="genomic Dl
                                                                                                                                                                                                                                                                                              Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                             Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BI378081
BI378081.1 GI:30913195
  (bases 1 to 888)
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                                                                                                                                                                                                              Tel: 301-838-5843
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BI378081/c
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אמס 13-SEP 2004 מאנו באנון אמס 13 bp BNA SSS 23-SEP-2004 ZMMBLa0012A22.f ZMMBLa Zea mays genomic clone ZMMBLa0012A22 5', genomic survey sequence.
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clone from which the above EST is generated is available at the amphioxus project site at: http://www.molgen.mpg.de/amphioxus/clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 843)
Wing.R., Luo,M., Soderlund,C. and Haller,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                    FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP)
Insert Length: 1200 Std Brror: 0.00
Seq primer: 5'-CCGGTCGGAATTCCCGGGT-3' pSport3/86
High quality sequence stop: 577.
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70.7%; Score 21.2; DB 4; Length 577;
Best Local Similarity 73.1%; Pred. No. 3.5e+02;
Matches 19; Conservative 4; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jurian Bequence (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Fal: 520 626 9595
                                                                                                                                                                                                                                                                                         /organism="Branchiostoma floridae"
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70.0%; Score 21; DB 5; Length 345;
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                                                                                                                                                                                                                                                                                               AW342249 21-JAN-2001 CHAESTI Guillardia theta Lambda Zap II cDNA Library Guillardia theta cDNA clone 38r, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="SOLR"
/clone_lib="Guillardia theta Lambda Zap II cDNA Library"
/note="Vector: Lambda ZAP II; Site_1: EcoRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                        SM Guillardia there

Eukaryote; Cryptophyta; Cryptomonadaceae; Guillardia.

E I (Dasse 1 to 214)

F raunholz, M., Duebel, J., Wastl, J., Zauner, S. and Maier, U.-G.

EST Database of the cryptomonad alga: Guillardia theta

Unpublished (2000)

Contact: Maier, U.-G.

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Tel: +49 6411 282 2057

Fax: +449 6412 282 1843

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Mus musculus cDNA clone L930183C02 5', mRNA sequence.
                                                                                                             Gaps
/note="Vector: pAGIBAC1; Site_1: Sal1; Site_2: Sal1"
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                                                             ch 70.7%; Score 21.2; DB 9; Similarity 73.1%; Pred. No. 3.7e+02; 19; Conservative 4; Mismatches 3;
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/strain="CCMP327"
/db_xref="taxon:55529"
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Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, R.S., Gasterland, T., Terrest, R.S., Garimond, S. Garimond, S. Garimond, S., Garimond, S., Kawaji, C., Godzik, A., Gough, J. Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Oxido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, J.C., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tonata, M., Verando, R., Wagner, L., Wahlestedt, C., Wang, Y., Waranabe, Y., Walling, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alzawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, M., Imctani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, B.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
Email: genome-reseasc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozanta, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakaume, N., Sastok, Satok, Satok, Sakai, K., Sakaume, N., Sastok, D., Satok, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
Genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1157-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse fissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/mol_type="mRNA"
/strain="C57BL/6J"
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clone="L930183C02"
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Matches

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

ACCESSION VERSION

DEFINITION

RESULT 9 CD296187

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Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP323621, genomic survey sequence. CR048521. GI:49781660 GSS, genome survey sequence, MICER. Mus musculus (house mouse)
                                                                                                                                                 BF103720 519 bp mRNA linear EST 19-OCT-2000 601647304F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931440 5',
                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCs
Colla Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM/67 row: h column: 01
High quality sequence stop: 518.
Location/Qualifiers
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Best Local Similarity 75.9%; Pred. No. 4.2e+02;
Matches 22; Conservative 2; Mismatches 5;
488 GAAAGGAACAAGAGCAGATTAAGCAGAGG 516
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                                                                                                                                                                                                                                                        BF103720.1 GI:10886246
                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                       mRNA sequence.
BF103720
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CR048521/c
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BF103720
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The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above BST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/ . cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MPWGpG91019122;MPI_SURUDI_122G19"
/tissue_type="whole larva"
/tissue_type="whole larva"
/tissue_type="whole larva"
/tissue_type="whole larva"
/lab_host="E.coli, XLI blue"
/clone lib="Sea urchin larva cDNA library MPMGp691"
/note="Wector: pSport1; Site_1: Not1; Site_2: Sal1; Random primed and directionally cloned in pSport1 vector using a Not1 (5'-pGACTAGATCGCAGGCGCCGCC (7)15-3' and a Sal1 5'- TCGACCCAGGCGTCGG-3'adapters (Gibco BRL)"
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(M13FSP) 3'-seq
                                                                                                                                                                                                                                                                                                                                                                                                                                              Strongylocentrous purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoidas;
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoidas;
Echinoidae; Euchinoidae; Echinoida;
Strongylocentrotidae; Strongylocentrotus.

1 (bases 1 to 399)
S Pouetka, J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Beck, A. Reinhardt, R., Herwig, R., Panopoulou, G. and Lehrach, H.
Generation, annotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters
Contact: Pouetka AJ 13(12), 2736-2746 (2003)
Contact: Pouetka AJ 13(12), 2736-2746 (2003)
Iaboraty 145, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr. 63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1128
                               Gaps
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BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP)
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
High quality sequence stop: 399.
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CDNA library MPMGp691
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Pred. No. 4e+02;
                                                                                                                                                                                                                                                                        StrPu691.007582 Sea urchin larva cDNA library MPMGF
Strongylocentrotus purpuratus cDNA clone
MPMGp691G19122,MPI_SURUDI_122G19 5', mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:7668"
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                            Indels
  Similarity 75.9%; Pred. No. 3.9e+02; 22; Conservative 2; Mismatches 5
                                                                                                          2; Mismatches
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                                                                           1 GACAUGAACAAGAGAUGAUUAGGCAGAGG
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CD296187.1 GI:34747264
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l Similarity 73.3%;
22; Conservative
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Query Match Best Local (

ORIGIN

FEATURES

Matches

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CC258547 1110 bp DNA linear GSS 13-MAY-2003
CH261-63K24_RM1.1 CH261 Gallus gallus genomic clone CH261-63K24,
                                                              98 GAAAGGAACAAGAGGTGAGAAGGCAGAGG 70
                                      GACAUGAACAAGAGAUGAUUAGGCAGAGG 29
                                                                                                                                                                                                                                                 genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                      Gallus gallus (chicken)
Gallus gallus
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BF342749
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Bases I to 880)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CLONE distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:

Localiny Sequence stop: 680.

Localiny Quality sequence stop: 680.

Localiny Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutleleostomi; Mammalia; Eutleria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 62). Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:471191"
/tissue_type="adrenal cortex carcinoma, cell line"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_hogt=="DH10B (phage-resistant)"
/clone_lib="NHH MGC 84"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
/noti="Grape insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG104640 880 bp mRNA linear EST 30-JAN-2001
602311331F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4421191 5',
                                                                                                                                                                      Hinxton, Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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1 Similarity 72.4%; Pred. No. 4.4e+02;
21; Conservative 3; Mismatches 5; Indels
                                                                                                                                                             Submitted (20-FEB-2004) Sanger Centre, HinxiCB10 1SA, UK. http://www.sanger.ac.uk/MICERLocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP23e21"
/clone_lib="MHPP"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                               Rogers, J. and Bradley, A. Direct Submission
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BG104640.1 GI:12598486
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1154 bp mRNA linear EST 22-NOV-2000 602015013F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150755 BF342749
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria; Aves; Neognathae, Galliformes; Phasianidae, Phasianidae, Baluae, Gallus.

1 (bases 1 to 1110)

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Garves, T., Mardis, E. and Wilson, R.
Gallus gallus BAC End Reads
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_line="UCD001, inbred 256"
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/note="Vector: pTABAC2.1; Site_l: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 1154)
11 HMG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                  Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                          Email: submissions@wätson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: EM1 TACGACTCACTATAGGGAGA
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .1110
/organism="Gallus gallus"
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/strain="Red Jungle Fowl"
/db_xref="texcon:9031"
/clone="CH261-63K24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 GAAATGAAGAAGAGATAAATAGGCACAGG 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 43
High quality sequence stop: 696.
Location/Qualifiers
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TITLE
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Gaps

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5; Indels

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S Zambrowicz, B.P.; Abuin, A.; Ramirez-Solis, R.; Richter, L.J.; Fighter, J. Button, E.C.; Edwards, J.; Finch, R.A.; Friddle, C.J.; Gupta, A.; Hansen, G.; Hu, Y.; Huang, W.; Jaing, C.; Key, B.W. Jr.; Kipp, P.; Kohlhauff, B.; Ma, Z.-O.; Markesich, D.; Payne, R.; Petter, D.G.; Qian, N.; Shaw, J.; Schrick, J.; Shi, Z.-Z.; Sparks, M.J.; Van Sligtenhorst, I.; Vogel, P.; Walke, W.; Xu, N.; Zhu, O.; Person, C. and Sands, A.T. Whal kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Conteact: Zambrowicz BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG623002 73 bp mRNA linear GSS 02-OCT-2003 OST323776 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST323776,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.lln.gov
Plate: LLAM9414 row: j column: 04
High quallity sequence stop: 657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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Best Local Similarity 69.0%; Pred. No. 4.7e+02;
Matches 20; Conservative 4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:4150755"
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Location/Qualifiers
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Mus musculus
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CG623002.1 GI:37446851
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DEFINITION
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CG623002
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               COMMENT
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/cell_type="embryonic stem cell"
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Gaps
                                       ó
Length 73;
                                         Indels
Query Match
69.3%; Score 20.8; DB 9;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 18; Conservative 4; Mismatches 5;
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Search completed: March 17, 2005, 11:07:42 Job time : 2082.4 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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March 17, 2005, 04:03:33 ; Search time 171.333 Seconds (without alignments) 691.020 Million cell updates/sec Run on:

US-08-901-612A-60 20

Title: Perfect score:

1 gacatgaacaagagatgatt 20 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

genesequ2002bs:*
genesequ2003as:*
genesequ2003bs:*
genesequ2003cs:*
genesequ2004as:*
genesequ2004as:* N_Geneseq_16Dec04:* 1: geneseqn1980s:* 2: geneseqn1990s:* 3: geneseqn2000s:* geneseqn2001as:*geneseqn2001bs:*geneseqn2002as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 20 | 100.0 | 36 | 12 | ADC64742 | Adc64742 Hepatitis | . E. |
| 20 | 100.0 | 87 | 4 | AAD09094 | Aad09094 Hepatitis | E |
| 20 | 100.0 | 129 | 4 | AAD09093 | Aad09093 Hepatitis | <u> </u> |
| 20 | 100.0 | 639 | 9 | AAD27422 | Aad27422 Hepatitis | F |
| 20 | 100.0 | 639 | 9 | AAD31509 | Aad31509 Hepatitis | <u>_</u> |
| 20 | 100.0 | 655 | 4 | AAH77569 | | ፎ |
| 20 | 100.0 | 655 | 4 | AAH77568 | Aah77568 HBV genot | E |
| 20 | 100.0 | 655 | 4 | AAH77574 | Aah77574 HBV genot | E |
| 20 | 100.0 | 655 | 4 | AAH77573 | Aah77573 HBV genot | E. |
| 20 | 100.0 | 655 | 4 | AAH77570 | Aah77570 HBV genot | <u>E</u> |
| 20 | 100.0 | 655 | 4 | AAH77571 | Aah77571 HBV genot | <u>.</u> |
| 20 | 100.0 | 664 | 4 | AAH77572 | Aah77572 HBV genot | Ď. |
| 20 | 100.0 | 699 | 12 | AD007220 | Ado07220 Hepatitis | Ĭ. |
| 20 | 100.0 | 673 | 4 | AAD09092 | Aad09092 Hepatitis | <u>-</u> |

modified base

| Aah77563 HBV preCo | | | Aav82687 Fulminant | Aav82692 Fulminant | _ | Aav82690 Fulminant | Aav82684 Fulminant | _ | _ | Aav82694 Fulminant | | - | Aav82689 Fulminant | Aav82693 Fulminant | Aan93072 Sequence | | Aaq04799 Recombina | Aah42375 Nucleotid | Aad31765 Hepatitis | Aca62422 Hepatitis | Aad60866 Hepatitis | Aaz88924 Hepatitis | Aad09091 Hepatitis | Aah77562 HBV genot |
|--------------------|----------|----------|--------------------|--------------------|----------|--------------------|--------------------|----------|----------|--------------------|----------|----------|--------------------|--------------------|-------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AAH77563 | AAH77567 | AAV82688 | AAV82687 | AAV82692 | AAV82685 | AAV82690 | AAV82684 | AAV82695 | AAV82683 | AAV82694 | AAV82686 | AAV82706 | AAV82689 | AAV82693 | AAN93072 | AAN00003 | AAQ04799 | AAH42375 | AAD31765 | ACA62422 | AAD60866 | AAZ88924 | AAD09091 | AAH77562 |
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| 675 | 681 | 1395 | 1400 | 1445 | 1445 | 1445 | 1445 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 2342 | 2743 | 2743 | 3180 | 3182 | 3182 | 3182 | 3220 | 3248 | 3248 |
| 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 |
| c 21 | c 22 | c 23 | C 24 | c 25 | c 26 | C 27 | c 28 | c 29 | c 30 | c 31 | c 32 | c 33 | c 34 | c 35 | c 36 | c 37 | c 38 | c 39 | c 40 | C 41 | c 42 | C 43 | C 44 | c 45 |

ALIGNMENTS

1. .20 /*tag= a /note= "Internucleotide linkages are phosphorothioate" Hepatitis B virus RNA antisense oligonucleotide HBV46MYb. HBV; HBV infection; inhibition; replication; ss. /*tag= c /mod_base= OTHER /note= "2'-O-methyladenosine" /*tag= e /mod_base= OTHER /note= "2'-0-methyladenosine" /*tag= h /mod_base= OTHER /note= "2'-0-methyladenosine" Location/Qualifiers BP. /*tag= b /mod_base= gm /*tag= d /mod_base= cm /*tag= f /mod_base= um /*tag= g /mod_base= gm AAT72566 standard; RNA; 20 (first entry) Key misc_feature modified base modified_base modified_base modified_base modified_base modified_base modified_base 03-SEP-1997 Synthetic. AAT72566; RESULT 1 AAT72566 ID AAT7 ö

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Indels

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Score 20; DB 2; Length 20; Pred. No. 9.6;

Sequence 20 BP; 9 A; 2 C; 5 G; 0 T; 4 U; 0 Other;

100.08;

ilarity 80.0%; Conservative

Local Similarity les 16, Conserv

Query Match Best Loc Matches

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Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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                     note= "2'-0-methyladenosine"
                                                                                                           *tag= 1
|mod_base= OTHER
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mod_base= OTHER
note= "2'-O-methyladenosine"
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mod_base= OTHER
not== "2'-O-methyladenosine"
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/note= "2'-O-methyladenosine"
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/*tag= i
/mod_base= OTHER
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Roberts PC,
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Roberts NA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a synthetic oligonucleotide HBV46Yb which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non-contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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/note= "Internucleotide linkages are phosphorothioate"
                Gaps
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                                                                                                                                                                                                                         Hepatitis B virus RNA antisense oligonucleotide HBV46Yb.
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4; Mismatches
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PC, Slade A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craig CJ, Frank BL,
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                                                                                                                                                                                                                                                                                                           Key
misc_feature
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                                                                                                              RESULT 2
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RESULT 3 AAT72562

The present sequence represents a synthetic oligonucleotide HBV46MYb which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two noncontiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection

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a
"Internucleotide linkages are phosphorothioate"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/note= "2'-0-methyladenosine"
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/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine'
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/*tag= b
/note= "2'-OMe RNA"
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/mod_base= OTHER
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/mod_base= cm
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/mod_base= gm
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/mod_base= gm
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/mod_base= um
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/mod_base= um
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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/note= "Internucleotide linkages are phosphorothioate"
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                                                                                                   Hepatitis B virus RNA antisense oligonucleotide HBV88b.
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                                                                                                                                   HBV; HBV infection; inhibition; replication; 88.
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Roberts NA, Roberts PC, Slade A;
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AAT72562 standard; DNA; 30 BP.
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misc_feature
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WO9639502-A1

12-DEC-1996

04-JUN-1996; 06-JUN-1995;

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contains a sequence which is complementary to at least two non-contiguous regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                             present sequence represents a synthetic oligonucleotide HBV-89b which
                                                                                      Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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"Internucleotide linkages are phosphorothioate"
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Pred. No. 9.9;
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                                                                                                                                                                                                                                                                                                                                                          Sequence 30 BP; 12 A; 3 C; 9 G; 6 T; 0 U; 0 Other;
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mod_base= OTHER
note= "2'-O-methyladenosine"
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/note= "2'-0-methyladenosine"
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/*tag= b
/note= "2'-OMe RNA"
      Slade A;
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/mod_base= gm
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mod_base=
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        Roberts NA, Roberts PC,
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AAT72617
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                                                                                                                                                                                                                                                                                                                                                                       Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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/note= "Internucleotide linkages are phosphorothioate"
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                                                                                                                                                                                                                                                                      Jupp R, Kilkuskie RE,
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100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 16; Conservative 4; Mismatches 0; Indels
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                                                                                                                                                                                                      (HOFF ) HOFFMANN LA ROCHE & CO AG F. (HYBR-) HYBRIDON INC.
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PC, Slade A;
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/mod_base= um
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Roberts NA, Roberts PC,
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Key misc_feature

Synthetic

04-SEP-1997

AAT72616;

RESULT 5

8 셤 04-JUN-1996;

36-JUN-1995;

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12-DEC-1996

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Gaps

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The present invention describes a method of screening for an antiviral agent by the protein-priming activity of hepatitis B virus (HBV) DNA polymerase. Also described is developing an antiviral agent with a high selectivity to HBV which can be used for high-throughput screening. The present sequence represents an RNA oligonucleotide which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening of antiviral agents by protein-priming activity of hepatitis virus DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                               screening; antiviral; hepatitis B virus; HBV; DNA polymerase;
                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus DNA polymerase related RNA oligonucleotide.
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Pred. No. 10;
                                                        ; Score 20; DB 2; Length 30;
Pred. No. 9.9;
4; Mismatches 0; Indels
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                            Sequence 30 BP; 12 A; 3 C; 9 G; 2 T; 4 U; 0 Other;
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in a cell or for the treatment of HBV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Min MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 12; 13pp; Korean.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOGA-) MOGAM BIOTECHNOLOGY INST
(VIRO-) VIROGEN CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 GACATGAACAAGAGATGATT 18
                                                                                                                                                                                                                                       ВР.
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100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                           Query Match
Best Local Similarity 80.0%;
Matches 16; Conservative 4
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                                                                                                                                                                                                                                       ADC64742 Btandard; RNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD09094 standard; DNA; 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jung SI, Kim YC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-309015/30.
                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Hepatitis B virus.
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                                                                                                                                                                                                                                                                    ADC64742;
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 SXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a synthetic oligonucleotide HBV-89Mb which contains a sequence which is complementary to at least two noncontiguous regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used, odetect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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mod_base= OTHER
'note= "2'-O-methyladenosine"
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/note= "2'-O-methyladenosine"
                                              note= "2'-0-methyladenosine"
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/note= "2'-O-methyladenosine"
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mod_base= OTHER
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base= o⊤HER
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mod_base= OTHER
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/mod_base= gm
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/mod_base= um
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/mod_base= um
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                  tag=
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12-DEC-1996

3 Craig ô

Gaps

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The present invention relates to hepatitis B virus (HBV) strain FRI,
genotype G DNA encoding Precore/Core protein, HBpol, envelope (PreSI,
FreS2 and surface antigen HBsAg) and HBX proteins. HBv genotype G nucleic
acids and polypeptides are useful for diagnosing, prognosing and treating
infections caused by HBV genotype G. They can be used in a vaccine to
treat or prevent HBV genotype G infection. The HBV genotype G derived
nucleic acids and antibodies are useful for detecting HBV genotype G in a
sample or diagnosis of HBV genotype G infection. The presence of HBV
genotype G statistically correlates with the presence of Inver damage
and/or liver cancer in the subject. The HBV genotype G core insert
peptide encoding nucleic acid is useful for designing monitoring assays
to study and predict the evolution of anti-HBs and anti-HBs antibodies
antibodies or antigens of HBV genotype G are useful for identifying a
stable inver disease caused by HBV genotype G. The present sequence is
a hepatitis B virus (HBV) strain FRI, genotype G DNA fragment encoding e
antigen (HBeAg)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.
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                                                      HBV genotype G; precore; HBpol; polymerase; envelope protein; preSl; preS2; surface antigen; HBsAg; HBX protein; vaccine; HBeAg; liver disease; hepatitis; liver cancer; HBcAg; core antigen; ds.
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                  Hepatitis B virus FR1 strain genotype G HBeAg DNA fragment
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les 20; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                      Schinazi R,
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                                                                                                                                      Hepatitis B virus
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Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.

Claim 5; Page 57; 84pp; English.

Fried M;

Zoulim F,

Van Geyt C,

De Gendt S,

Schinazi R,

Stuyver L,

Rossau R;

WPI; 2001-367676/38.

21-NOV-2000; 2000WO-US032108

Hepatitis B virus.

WO200138498-A2

31-MAY-2001

99US-0167206P

24-NOV-1999;

(PHAR-) PHARMASSET INC. (INNO-) INNOGENETICS NV

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The present invention relates to hepatitis B virus (HBV) strain FR1, genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreS1, PreS2 and sutface antigen HBBAG) and HBX proteins. HBV genotype G nucleic acids and subsections are useful for diagnosing, prognosing and treating infections caused by HBV genotype G. They can be used in a vaccine to infection caused by HBV genotype G infection. The HBV genotype G derived nucleic acids and antibodies are useful for detecting HBV genotype G infection. The HBV genotype G infection. The presence of HBV genotype G infection. The presence of HBV can proposed of a sample or diagnosis of HBV genotype G infection. The presence of liver damage and/or liver cancer in the subject. The HBV genotype G core insert peptide encoding nucleic acid is useful for designing monitoring assays to study and predict the evolution of anti-HBe and anti-HBc antibodies to antibodies or antigens of HBV genotype G are useful for identifying a stage of liver disease caused by HBV genotype G. The present sequence is a hepatitis B virus (HBV) strain FR1, genotype G DNA fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus; HBV; core antigen; HBCAg; immune system; typhoid; prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes; hepatitis C virus; HCV; influenza; foot-and-mouth disease; diarrhoes; tuberculosis; pollo; rables; acquired immunodeficiency syndrome; AIDS; dengue fever; yellow fever; malaria; whooping cough; salmonellosis; food poisoning; meningitis; gonorrhea; antiviral; antibacterial; antiprotozoal; ds.
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Best Local Similarity 100.
Matches 20, Conservative
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Hepatitis B virus

HBV genotype G; precore; HBpol; polymerase; envelope protein; preSl; preS2; surface antigen; HBsAg; HBX protein; vaccine; liver disease; hepatitis; liver cancer; HBcAg; core antigen; ds.

Hepatitis B virus FR1 strain genotype G DNA fragment #1.

04-SEP-2001 (first entry)

AAD09093;

BP.

AAD09093 standard; DNA; 129

AAD09093/ RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to modified proteins comprising hepatitis B virus (HBV) core antigen (HBCAg) wherein one or more of the four arginine repeats has been deleted and the protein comprising the C-terminal cysteine of HBCAg. The deleted region may be replaced by an epitope from a protein other than HBCAg, in which case the HBCAg acts as a carrier to present the epitope to the immune system. This chimeric protein or its nucleic acid is useful as a vaccine or in a method of prophylactic or therapeutic vaccination of the human or animal body, particularly against HBV. The nucleic acid encoding the protein may be used in gene therapy or DNA vaccination protocols. The chimeric protein or its nucleic acid may also be used as the basis of a prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth disease, polio, herpes, rabise, acquired immunodeficiency syndrome (AIDS), dengue fever, yellow fever, malaria, tuberulosis, whooping cough, salmonallosis, typhoid, food poisoning, diarrhoea, meningitis or gonorrhea. The present sequence is a DNA chocking Hepatitis B virus core antigen (HBCAG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New proteins comprising a modified hepatitis B core antigen, useful as a vaccine in prophylactic or therapeutic vaccination of the human or animal body, particularly against hepatitis B virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus core antigen; HBcAg; prophylactic; viral hepatitis; therapeutic; vaccine; acquired immune deficiency syndrome; influenza; polio; herpes; rabies; AIDS; foot-and-mouth disease; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Location/Qualifiers
1. .639
                                                                   /product= "HBcAg"
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                                                                                                                                                                                                           22-JUN-2001; 2001WO-GB002817
                                                                                                                                                                                                                                                      22-JUN-2000; 2000GB-00015308
06-OCT-2000; 2000GB-00024544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD31509 standard; DNA; 639
                                                                                                                                                                                                                                                                                                                             (CELL-) CELLTECH PHARM LTD.
                                                                                                                                                                                                                                                                                                                                                                           Li J, Pumpens P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-2002 (first entry)
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P-PSDB; AAE17018.
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Best Local Similarity
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                                                                                                               WO200198333-A2
                                                                                                                                                             27-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                        Page M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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The present invention relates to hepatitis B virus (HBV) core antigen (HBCAG) fusion proteins and polymucleotides encoding such proteins. Sequences of the invention are useful in methods of prophylactic or therapeutic vaccination or manufacture medicaments for prophylactic or therapeutic vaccination of the human or animal body against HBV, e.g. against viral hepatitis. They are also useful as a prophylactic vaccine against e.g. hepatitis c virus, influenza, polio, herpes, rabies, acquired immune deficiency syndrome (AIDS) or foot-and-mouth disease. The present sequence is a DNA encoding hepatitis B virus core antigen (HBCAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis B (HB) core antigen fusion proteins, useful as vaccines for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylactic or therapeutic treatment of humans or animals against e.g. HB virus, viral hepatitis, hepatitis C virus, influenza, or foot-andmouth disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus; HBV; preCore; Core; preSl; preS2; HBS; HBX; HBPol;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;
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                                                                                                                                                 /product= "Mature HBc protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rowlands D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HBV genotype G strain US1 preCore/Core DNA.
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/*tag= a
/product= "HBc protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH77569 standard; DNA; 655 BP
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                                                                                                                                                                                                                                                                                                        09-APR-2001; 2001WO-GB001607
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                                             1. .87
/*tag= b
88. .636
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilbert R,
                                                                                                                                                                                                                                                                                                                                                                                                          (MEDE-) MEDEVA EURO
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                                                  sig_peptide
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from HBV

therapy

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sample. Ligands that bind to the proteins and antibodies directed against the proteins are useful for detecting the proteins and for detecting HBCAG and HBCAG (precore precursor proteins). They are also useful for preparing a vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/Core sequences of an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FR2, US1, US3, US6, US7, US9, US10) of HBV genotype G
                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBV genotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies in a biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis B virus; HBV; preCore; Core; preSl; preS2; HBS; HBX; HBPOl;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
                                                                                                       Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 4; Length 655; 100.0%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                             Claim 3; Fig 7; 94pp; English.
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                                 WPI; 2001-374785/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH77574;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the UGA. The invention relates to a fully defined sequence of 3248 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or specification, a sequence with 92% identity to the given sequence, or olynucleotides are useful for HBW genotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies directed against the proteins are useful for the proteins and for detecting the proteins and for detecting the proteins and for detecting the proteins and vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/Core sequences of an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FRZ, USI, US3, USG, US7, US9, USIO) of HBV genotype G
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AAH77568/C
ID AAH77568 standard; DNA; 655 BP
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AC AAH77568;
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DT 19-OCT-2001 (first entry)
XX
DE HBV genotype G strain FR2 precorner of the Base of th
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                        99EP-00870252.
99US-0169287P.
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                                                                                                                                        (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                  Stuyver L, Van Geyt C,
                                                                                                                                                                                                                                                                                                WPI; 2001-374785/39.
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Best Local Similarity
                        03-DEC-1999;
07-DEC-1999;
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Matches

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Gaps

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0; Indels

HBV

Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from genotype A-F molecules, useful for HBV diagnosis, prophylaxis and

therapy

De Gendt S;

WPI; 2001-374785/39.

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This genotype was found with a high prevalence in patients fortonically infected with HBV and residing in Europe and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequence. These polynucleotides are useful for HBV genotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins and antibodies directed against the proteins are useful for detecting the proteins and for detecting the proteins and for detecting reparing a vaccine or medicament for treating HBV infections. The preparing a vaccine or medicament for treating HBV infections. The an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FRZ, USI, USS, USI, USS, USI, USS).
                                                                                 invention relates to the complete nucleic acid sequence of a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;
                          Claim 3; Fig 7; 94pp; English
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100.0%; Score 20; DB 4; Length 655; 100.0%; Pred. No. 13; 0; Indels 0; Mismatches 20 1 GACATGAACAAGAGATGATT 20; Conservative Local Similarity Query Match Matches

43 GACATGAACAAGAGATGATT 24 a ઠે

AAH77573 standard; DNA; 655 AAH77573;

В

HBV genotype G strain US7 preCore/Core DNA. 19-OCT-2001 (first entry)

Hepatitis B virus; HBV; preCore; Core; preSl; preS2; HBS; HBPOl; HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg; HBeAg; ds.

Hepatitis B virus.

WO200140279-A2

07-JUN-2001.

20-NOV-2000; 2000WO-EP011526.

99EP-00870252 03-DEC-1999; 07-DEC-1999;

(INNO-) INNOGENETICS NV

Gendt S;

De

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Van Geyt

Stuyver L,

WPI; 2001-374785/39.

Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and therapy

Claim 3; Fig 7; 94pp; English.

The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Burope and the USA. The invention

relates to a fully defined sequence of 3248 nucleotides as given in 888888888888888

Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

Gaps ó, Score 20; DB 4; Length 655; Pred. No. 13; Indels o; Mismatches 100.0%; Scor 100.0%; Pre Query Match 100. Best Local Similarity 100. Matches 20; Conservative

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1 GACATGAACAAGAGATGATT 20 24 43 GACATGAACAAGAGATGATT ద

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Search completed: March 17, 2005, 06:48:41 Job time : 171.333 secs

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Gaps

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Gaps

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SOURCE

ACCESSION

VERSION KEYWORDS

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

CG381984/c DEFINITION

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CG373225 892 bp DNA linear GSS 26-AUG-2003 OG1CZ28TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0734E08,
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Mittelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Unpublished (2002)
Other_GSSs: OGICZ28TH
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methylation filtered genomic DNA library"
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9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 946
/organism="Zea mays"...
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95.0%; Pred. No. 4.3e+02;
tive 0; Mismatches 1;
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/strain="B73"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TF
Class: sheared ends.
Location/Qualifiers
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CG373225
CG373225.1 GI:34290492
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Best Local Similarity
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COMMENT
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CG373225
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
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Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R. W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
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                                                                                   OGIBK24TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0724C23, genomic survey sequence.
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OG1CZ28TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0734E08,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
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methylation filtered genomic DNA library"
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92.0%; Score 18.4; DB 9; Length 773;
Best Local Similarity 95.0%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels
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Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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Contact: Cathy Whitelaw
TIGR
                                                                                                                                                                                             CG381984.1 GI:34299251
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RESULT 3 CG373212/c LOCUS

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SOURCE ORGANISM

KEYWORDS

ACCESSION

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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Gaps

353 GGCATGAACAAGAGATGATT 372

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Submitted Jan. 13. Mar. 2004) Weisshaar B., Max-Planck-Institut fuer Submitted (31-MAR. 2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone fast33. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for Elanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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                                                   BX288914 280 bp DNA linear GSS 02-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-421D09-018141,
                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                      Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis
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/ecotype="Col-0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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Pred. No. 1.1e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis thaliana"
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Arabidopsis thaliana
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94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
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Gaps

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Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H. Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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                                                                                                                                     EST 15-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                             annuum L.) and Sequence Analysis in Relation to Hypersensitive annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen Unpublished (2001)
Contact: Doil Choi Genome Research Center and National Center for Genome Information Korea Research Institute of Bioscience and Biotechnology P.O. Box 115, Yusong, Taejeon, 305-600, Republic of Korea Tel: 82-42-860-4340
Fax: 82-42-860-4309
Fax: 82-40-860-4309
                                                                                                                                                                                                                                                              Capsicum annuum
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Capsicum.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 305)
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S.,
Hur, C.-G. and Choi, D.
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A0504F09-5 NIA Mouse Mesenchymal Stem Cell CDNA Library (Longmus musculus CDNA clone NIA:A0504F09 IMAGE:30743204 5', mRNA
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KSllolyBl2 KSll Capsicum annuum CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Capsicum annuum"
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/db_xref="taxon:4072"
/clone lib="KS11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCWV-SPORT6 (Invitrogen); Site 1: Sall; Site 2: Not1; Mouse cDNA project by the Laboratory of Genetics. National Institute on Asing (NIA), Intramural Research Program, NIH (http://logun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 153-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Akihiro Umczawa (Keio University School of Medicine, Japan). Double-stranded cDNAs were synthesized with an Oligo (dT) primer
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1 (bases 1 to 423)
Castelli, V. Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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/dev_stage="9-15C cells"
/lab_host="DH10B"
/clone lib="NIA Mouse Mesenchymal Stem Cell cDNA Library
(Long I)"
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National Institute on Aging/National Institutes of Health 313 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdmal Drive, Surc.nia.nih.gov Plate: A0504 row: F column: 09 Seq primer: M13 Reverse High quality sequence stop: 313 POLYANNO.
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87.0%; Score 17.4; DB 7; Length 313;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="C3H/He mice"
/db_xref="niaEST:A0504F09-5"
/db_xref="taxon:10090"
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Genoscope - Centrer National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequences cons.fr, Web : www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraties construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ183243 120 MR CIT Approved Human Genomic Sperm Library D Homo saplens genomic clone Plate=3140 Col=4 Row=D, genomic survey
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 426)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Hormone Treated Callus"
/dlone_lib="Arabidopsis thaliana Hormone Treated Callus
Col-0"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
191: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Arabidopsis thaliana"
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/clone="GSLTPGH21ZC04"
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Plate: 3140 row: D column: 4
Class: BAC ends
High quality sequence stop: 426.
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/ecotype="Col-0"
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Unpublished (2004)
Contact: Genoscope
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Matches 18; Conservative
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Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114] gb|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptore complementary to the insert adaptore and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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                                                                                Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mumanlas, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 450)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longarre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Stokes,R., Tingey,A., von
Niederhauserrn,A. and Wright,D., Weiss,R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0528 row: D column: 16
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0528D16"
                                                                    Mus musculus (house mouse)
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Fax: 801 585 7177
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Contact: Crawford, Douglas L.
Marine Genomics - Crawford Lab
Rosenstiel School of Marine and Atmospheric Science - University of
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Fundulus heteroclitus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Fundulidae; Fundulus.
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Crawford,D.L., Oleksiak,M.F., Kolell,K.J., Paschall,J., VanWye,J.,
Road,J.L. and Whitchead,J.A.
Fundulus Functional Genomics: EST Database for Teleost Fish
                                                                                                                                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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http://genomics.rsmas.miami.edu/funnybase/super_craw3/
Plate: 100122 row: B column: 6.
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Tel: 305 361 4121
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/clone Tib="Fundulus Heteroclitus Liver"
/note="Organ: Liver"
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/organism="Fundulus heteroclitus"
               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_rzref="taxon:9606"
/clone="plate=3140 Col=4 Row=D"
/sex="male"
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/db_xref="taxon:8078"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Nishino, H., Tashiro, H., Jazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshikagi, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN Integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length corAs
Nature 420, 563-573 (2002)
6 (Dases I to 509)
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                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             he RIKEN Genome Exploration Research Group Phase II Team and the
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                                                                                                                                     Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9927923
10349636
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AK015232.1 GI:12853489
HTC; CAP trapper.
Mus musculus (house mouse)
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COMMENT

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/tissue_type="testis"
/clone lib="RIKEN full-length enriched mouse cDNA library"
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1. .509
/note="unclassifiable"
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,
Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Unpublished (2000)
Unpublished (2000)
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="C57BL/G1"
/db_xref="FANTOM_DB:4930429C20"
/db_xref="taxon:10090"
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94.7%; Pred. No. 1...
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1. .527
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AQ961278
AQ961278.1 GI:6788979
                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                              1. .509
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/notes_vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall;
Site_2: NotI; Mouse cDNA project by the Laboratory of
Genefice, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAS were obtained from Dr. Akihiro Umezawa (Keio
University School of Medicine, Japan). Double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIA Mouse Mesenchymal Stem Cell cDNA Library [Long 1] "
                                                               Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
National Institute 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsuu.grc.nia.nih.gov
Plate: A0536 row: H column: 03
Seg primer: M13 Reverse
High quality sequence stop: 574
POLYA-NO.
                                                                                                                                                                                                                                                                                                                                                       /db_xrefe="niaegr:A0536H03-5"
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                                                                                                                                                                                                                                              Location/Qualifiers
                                            Contact: Dawood B. Dudekula
  21429098
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PUBMED
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                                                                                                                ö
                                                                                                                                                                                                                                                                                                               CP198522 S70 bp mRNA linear EST 01-AUG-2003
EST0117 Tamarix androssowii leaf Tamarix androssowii cDNA, mRNA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Caryophyllales; Tamaricaceae; Tamarix.

(bases 1 to 570)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang, Y., Yang, C., Jiang, J., Liu, G., Wu, J. and Liu, Z. EST aguired from cDNA library of Tamarix androssowii treated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CF909462 1.00 S74 bp mRNA linear EST 05-NOV-2. A0536H03-5 NIA Mouse Mesenchymal Stem Cell cDNA Library (Long 1) Mus musculus cDNA clone NIA:A0536H03 IMAGE:30746294 5', mRNA
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                                                                   Length 527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yucheng Wang
Forestry Source and Environment College
Northeast Forestry University
Hexing 26, Harbin, Heilongjiang, 150040, P.R. China
Tel: 086-451-2190607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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  sheared to 0.9-1 Kbp before ligation."
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/tissue type="leaf"
/clone_lib="Tamarix androssowii leaf"
                                                                 Query Match

87.0%; Score 17.4; DB 8;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1;
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/organism="Tamarix androssowii"
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94.7%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: WANGYUCHENG1029@YAHOO.COM.CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                 160 ACATGAACAAGAGAAGATT 142
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CP909462/c
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                                                                                                                                                                                          510 GAAATGAACAAGAGATGAT 492
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Matches 18; Conserv?
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Hepatitis Hepatitis

Hepatitis Hepatitis

AF528232 AF528233 AF528234 AF528235

AF528236 Hepatitis AF528237 Hepatitis

Hepatitis

AF528214 AF528215 AF528216 AF528210 AF528210 AF528220 AF528221 AF528221 AF528221 AF528225 AF528225 AF528225 AF528225 AF528225 AF528225 AF528225 AF528225 AF52823

nucleic

Run on:

Sequence:

Searched:

Database

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Unclassified.
1 (bases 1 to 30)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
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11 (bases 1 to 30)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
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Oligonucleotides specific for hepatitis B Patent: US 5856459-A 8 05-JAN-1999;
Location/Qualifiers
1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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Sequence 39 from patent US 5856459.
AR027841.1 GI:5938661
                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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Sequence 8 from patent US 5856459.
AR027810 GI:5938630
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AF528215
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Unknown.
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AF528205 Hepatitis
AF528207 Hepatitis
AF528207 Hepatitis
AF528208 Hepatitis
AF528209 Hepatitis
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AR121115 Sequence
AX151115 Sequence
M7668 Heparitis B
M7669 Heparitis B
                                                                                          March 17, 2005, 04:07:57; Search time 683.733 Seconds (without alignments) 1417.372 Million cell updates/sec
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                                                                                                                                                                                                                                                                             9416466
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                4708233 segs, 24227607955 residues
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Query Match Best Local &

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RESULT 3 AX151115/c LOCUS

DEFINITION ACCESSION VERSION KEYWORDS

ORGANISM

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REFERENCE AUTHORS

source

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FEATURES TITLE

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HPBPRECB 11-MAY-1994 Hepatitis B virus type 2precore protein (pre-C region, C) gene, 5'
                                                                                                                                                                                                                                                                           /note="g in wt; a in virus type 1 (creates internal stop codon)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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note="g in wt; a in virus type 2 (creates internal
codon)"
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                                                                                                           /gene="C"
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100.0%; Score 20; DE
Best Local Similarity 80.0%; Pred. No. 50;
Matches 16; Conservative 4; Mismatches
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            /mol_type="genomic DNA"
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/gene="C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and Will,H.
                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                      DB 6; Length 30;
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Mills,J.S.
Oligonucleotides specific for hepatitis B virus
Patent: US 5856459-A 39 05-JAN-1999;
Location/Qualifiers
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Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
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                                                                                    1. .30
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Sequence 4 from Patent WO0138498.
AX151115
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Matches 16; Conservative
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Query Match

DRIGIN

RESULT 4 HPBPRECA/c LOCUS ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE

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FEATURES

JOURNAL

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Gaps

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JOURNAL MEDLINE

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HPBPRECE 11-MAY-1994 Heppetitis B virus type 5 precore protein (pre-C region, C) gene, 5'
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Hepatitis B virus
I (bases I to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and Will,H.
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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                         Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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                                                                                                                          source text: Hepatitis B virus DNA. Location/Qualifiers
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/db_xref="taxon:10407"
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/gene="C"
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/gene="C"
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/mol_type="genomic DNA"
/db_xref="taxon:10407"
/o. .93
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Hepatitis B virus type 4 precore protein (pre-C region, C) gene, 5'
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/note="g in wt; a in virus type 3 (creates internal stop
codon)"
                                                                                                                                                                                                                                         e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (Dases I to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area 91306476
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1 (bases 1 to 99)
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/note="g in wt; t in virus type 3 (val to phe)"
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/standard_name="pre-C region"
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Hepatitis B virus
Hepatitis B virus
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                   GACAUGAACAAGAGAUGAUU 20
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M76689.1 GI:485345
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/gene="C"
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HPBPRECC/c
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HPBPRECH 11-MAY-1994 By DNA linear VRL 11-MAY-1994 Hepatitis B virus type 8 precore protein (pre-C region, C) gene, 5'
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/note="g in wt; a in virus type 7 ( creates internal stop
codon)"
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Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and Will,H.
Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area virology 183 (2), 840-844 (1991)
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Hepatitis B virus
Hepatitis P virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area 91306476
                                                                                                                                                                                                                                                                                                                                                                                                                        'product="precore protein"
'øtandard_name="pre-C region note: putative CDS"
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Location/Qualifiers
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10..93
/gene="C"
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/gene="C"
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/db_xref="taxon:10407"
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80.0%; Pred. No. 50;
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52 GACATGAACAAGAGATGATT 33
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                                                                                            /gene="C"
/note="g in wt; a in virus type 5 (creates internal stop
codon)"
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/note="t in wt; c in virus type 6 (loss of start codon)"
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Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.

1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and Will, H.
Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area virology 183 (2), 840-844 (1991)
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/gene="C"
/note="gcc in wt; ccg in virus type 5 (ala to pro)"
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Location/Qualifiers
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10.-99
/gene="C"
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100.0%; Score 20; DB
Best Local Similarity 80.0%; Pred. No. 50;
Matches 16; Conservative 4; Mismatches
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/note="putative cds"
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52 GACATGAACAAGAGATGATT 33
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M76692.1 GI:485351
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HPBPRECG/c
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M76693.1 GI:485352

ACCESSION VERSION

DB 14; Length 99; Indels us-08-901-612a-61.rge

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HPBPRECM 99 bp DNA linear VRL 11-MAY-1994
Hepatitis B virus type 13 precore protein (pre-C region, C) gene,
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Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                                                                                                                                         Will,H.
Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area 91306476
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/note="g in wt; a in virus type 13 (gly to asp)
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Pred. No. 50;
4; Mismatches 0; Indels
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A new genotype of hepatitis b virus Patent: WO 0138498-A 3 31-MAY-2001; Pharmasset, Inc. (US) ; INNOGENETICS N.V.
Location/Qualifiers

    .129
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Sequence 3 from Patent WO0138498.
AX151114
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lee 16; Conservative 4;
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Hepatitis B virus type 9 precore protein (pre-C region, C) gene, 5'
                                                                                                  /gene="C"
/note="g in wt; a in virus type 8 (creates internal stop
codon)"
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/note="c in wt; t in virus type 9 (creates internal stop
codon)"
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Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and Will,H.
Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area
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10. .93
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80.0%; Pred. No. 50;
tive 4; Mismatches
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100.0%; Score 20; DE
Best Local Similarity 80.0%; Pred. No. 50;
Matches 16; Conservative 4; Mismatches
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                                                                 /gene="C"
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

I (Dases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
Unpublished
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
L Submitted (11-UUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411001, India
                                                      ö
                                                                                                                                                                                                                                               AF528205 150 bp DNA linear VRL 31-JUL-2003
Hepatitis B virus ASC1123 core antigen precursor, gene, partial
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/note="contains partial basal core promoter"
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/note="contains complete precore region"
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/mol type="genomic DNA"
/isolate="ASC1123"
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Search completed: March 17, 2005, 08:14:16 Job time : 683.733 secs

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'*tag= a
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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Aar72616 Hepatitis
Aar72617 Hepatitis
Aac64742 Hepatitis
Aac64742 Hepatitis
Aac67422 Hepatitis
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Aac6756 HBV Genot
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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The present sequence represents a synthetic oligonucleotide HBV46MYb which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two noncontaining a regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
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                     note= "2'-0-methyladenosine"
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mod_base= OTHER
note= "2'-O-methyladenosine"
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PC, Slade A;
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mod_base= OTHER
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Roberts PC,
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Roberts NA,
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/note= "Internucleotide linkages are phosphorothioate"
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            Sequence 20 BP; 9 A; 2 C; 5 G; 0 T; 4 U; 0 Other;
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RESULT 3

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/note= "2'-O-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/note= "2'-0-methyladenosine'
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/mod_base= OTHER
/note= "2'-0-methyladenosine'
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/*tag= b
/note= "2'-OMe RNA"
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/mod_base= OTHER
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/mod_base= OTHER
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/mod_base= um
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/mod_base= gm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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Pred. No. 9.9;
4; Mismatches 0; Indels
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                                                                                                 Hepatitis B virus RNA antisense oligonucleotide HBV88b.
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                                                                                                                                  HBV; HBV infection; inhibition; replication; ss.
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Roberts NA, Roberts PC, Slade A;
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AAT72562 standard; DNA; 30 BP.
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Best Local Similarity 80.0%;
Matches 16; Conservative
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misc_feature
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contains a sequence which is complementary to at least two non-contiguous regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                        The present sequence represents a synthetic oligonucleotide HBV-89b which
                                                                                   o:nucleotide(s) complementary to hepatitis B virus (HBV) sequences in the detection and treatment of HBV infection.
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"Internucleotide linkages are phosphorothioate"
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/mod base= OTHER
/note= "2'-O-methyladenosine"
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mod_base= OTHER
note= "2'-0-methyladenosine"
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/note= "2'-OMe
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Best Local Similarity 80.0°
Matches 16; Conservative
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    Roberts NA, Roberts PC,
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                                                                                 Oligo: nucleotide (8)
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                                                                                                                                                                                                                                                                                                                                                                      Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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/note= "Internucleotide linkages are phosphorothioate"
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Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels
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Roberts NA, Roberts PC, Slade A;
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misc_feature
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The present invention describes a method of screening for an antiviral agent by the protein-priming activity of hepatitis B virus (HBV) DNA polymerase. Also described is developing an antiviral agent with a high selectivity to HBV which can be used for high-throughput screening. The present sequence represents an RNA oligonucleotide which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening of antiviral agents by protein-priming activity of hepatitis virus DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                          screening; antiviral; hepatitis B virus; HBV; DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus DNA polymerase related RNA oligonucleotide.
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                                                                 Score 20; DB 2; Length 30;
Pred. No. 9.9;
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                                 Sequence 30 BP; 12 A; 3 C; 9 G; 2 T; 4 U; 0 Other;
 in a cell or for the treatment of HBV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ryu WS,
                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOGA-) MOGAM BIOTECHNOLOGY INST. (VIRO-) VIROGEN CO LTD.
                                                                                                                                      1 GACAUGAACAAGAGAUGAUU 20
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                                                                                                                                                                                                                                                         BP.
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                                                                   Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
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ID AAD09094 standard; DNA; 87
                                                                                                                                                                                                                                                       ADC64742 standard; RNA; 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
Hepatitis B virus.
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                                                                                                                                                                                                                                                                                         ADC64742;
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                                                                                                                                                                                                                                     ADC64742/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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                                                   'note= "2'-0-methyladenosine"
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/note= "2'-0-methyladenosine"
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nod_base= OTHER
                                                                                                                                    '*tag= l
'mod base= OTHER
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mod base= OTHER
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/mod_base= gm
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/mod_base= cm
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mod_base= gm
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/mod_base= um
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Roberts PC,
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Roberts NA,
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The present invention relates to hepatitis B virus (HBV) strain FR1, genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreS1, PreS2 and surface antigen HBsAg) and HBx proteins. HB yenotype G nucleic acids and surface antigen HBsAg) and HBx proteins. HBV genotype G nucleic acids and polypeptides are useful for diagnosing, prognosing and treating infections caused by HBV genotype G. They can be used in a vaccine to treat or prevent HBV genotype G infection. The HBV genotype G darived nucleic acids and antibodies are useful for detecting HBV genotype G in a sample or diagnosis of HBV genotype G infection. The presence of HBV genotype G statistically correlates with the presence of luver damage and/or liver cancer in the subject. The HBV genotype G core insert to study and predict the evolution of anti-HBC and anti-HBC antibodies and HBAQ (genotype G antigen) in patients infected with HBV. The antibodies or antigens of HBV genotype G are useful for identifying a stage of liver disease caused by HBV genotype G DNA fragment encoding e antigen (HBCAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.
                                                           HBV genotype G; precore; HBpol; polymerase; envelope protein; preSl; preS2; surface antigen; HBsAg; HBX protein; vaccine; HBeAg; liver disease; hepatitis; liver cancer; HBcAg; core antigen; ds.
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                       Hepatitis B virus FR1 strain genotype G HBeAg DNA fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Van Geyt C,
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                                                                                                                                                                                                                                                                                                          24-NOV-1999; 99US-0167206P
                                                                                                                                                                                                                                                                                                                                                 (PHAR-) PHARMASSET INC. (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                                                                                                                               Schinazi R,
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                                                                                                                                            Hepatitis B virus
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Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.

5; Page 57; 84pp; English.

Claim

Zoulim F, Fried M;

De Gendt S, Van Geyt C,

Schinazi R,

Stuyver L,

Rossau R;

WPI; 2001-367676/38.

(PHAR-) PHARMASSET INC. (INNO-) INNOGENETICS NV

21-NOV-2000; 2000WO-US032108

Hepatitis B virus.

WO200138498-A2

31-MAY-2001

99US-0167206P

24-NOV-1999;

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The present invention relates to hepatitis B virus (HBV) strain FRI, genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreSI, PreS2 and surface antigen HBsAg) and HBX proteins. HB yearouype G nucleic acids and polypeptides are useful for diagnosing, prognosing and treating infections caused by HBV genotype G. They can be used in a vaccine to treat or prevent HBV genotype G infection. The HBV genotype G derived nucleic acids and antibodies are useful for detecting HBV genotype G in a sample or diagnosis of HBV genotype G infection. The presence of HBV genotype G infection in the presence of liver damage and/or liver cancer in the subject. The HBV genotype G core insert peptide encoding nucleic acid is useful for designing monitoring assays to study and predict the evolution of anti-HBe and anti-HBC antibodies and HBAGA (genotype G antigen) in patients infected with HBV. The antibodies or antigens of HBV genotype G are useful for identifying a stage of liver disease caused by HBV genotype G DNA fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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100.0%; Score 20; Di
Best Local Similarity 80.0%; Pred. No. 11;
Matches 16; Conservative 4; Mismatches
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AAD27422 standard; DNA; 639
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16; Conservative

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Local Similarity

AAD09093 standard; DNA; 129 BP

HBV genotype G; precore; HBpol; polymerase; envelope protein; preSl; preS2; surface antigen; HBsAg; HBX protein; vaccine; liver disease; hepatitis; liver cancer; HBcAg; core antigen; ds.

Hepatitis B virus FR1 strain genotype G DNA fragment #1.

04-SEP-2001 (first entry)

AAD09093/ ID AAD0 XX AAD0 XX AAD0 DT 04-S DE HEPA XX HBV KW HBV KW Pres

AAD09093;

Key

Page M,

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The present invention relates to hepatitis B virus (HBV) core antigen (HBCAG) fusion proteins and polymucleotides encoding such proteins. Sequences of the invention are useful in methods of prophylactic or therapeutic vaccination or to manufacture medicaments for prophylactic or therapeutic vaccination of the human or animal body against HBV, e.g. against viral hepatitis. They are also useful as a prophylactic vaccine against e.g. hepatitis c virus, influenza, polio, herpes, rabies, acquired immune deficiency syndrome (AIDS) or foot-and-mouth disease. The present sequence is a DNA encoding hepatitis B virus core antigen (HBCAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B (HB) core antigen fusion proteins, useful as vaccines for the prophylactic or therapeutic treatment of humans or animals against e.g. HB virus, viral hepatitis, hepatitis C virus, influenza, or foot-and-mouth disease.
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                                                                                                                                        /product= "Mature HBc protein"
                                                                                                                                                                                                                                                                                                                                                                                                   Stuart D, Rowlands D;
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80.0%; Pred. No. 13;
               /*tag= a
/product= "HBc protein"
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43 GACATGAACAAGAGATGATT 24
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88. .636
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Best Local Similarity 80.09
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                                                                                                                                                                                                                                                                                                                                                         (MEDE-) MEDEVA BURO
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                                                                                                                                                                                                                                                                                                                                                                                                   Gehin A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to modified proteins comprising hepatitis B virus (HBV) core antigen (HBCAG) wherein one or more of the four arginine repeats has been deleted and the protein comprising the C-terminal cysteine of HBCAG. The deleted region may be replaced by an epitope from a protein other than HBCAG, in which case the HBCAG acts as a carrier to present the epitope to the immune system. This chimeric protein or its nucleic acid is useful as a vaccine or in a method of prophylactic or therapeutic vaccination of the human or animal body, particularly against HBV. The nucleic acid encoding the protein may be used in gene therapy or DNA vaccination protocols. The chimeric protein or its nucleic acid may also be used as the basis of a prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth disease, pollo, herpes, rabies, acquired immunodeficiency syndrome (ADS), dengue fever, yellow fever malaria, diarrhoea, meningitis or gonorrhea. The present sequence is a DNA encoding Hepatitis B virus core antigen (HBCAG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      New proteins comprising a modified hepatitis B core antigen, useful as a vaccine in prophylactic or therapeutic vaccination of the human or animal body, particularly against hepatitis B virus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus core antigen (HBcAg) encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; DE
80.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 38-39; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
Location/Qualifiers
                                     /*tag= a
/product= "HBcAg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACAUGAACAAGAGAUGAUU 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 GACATGAACAAGAGATGATT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD31509 standard; DNA; 639 BP.
                                                                                                                                                                                    22-JUN-2001; 2001WO-GB002817
                                                                                                                                                                                                                              22-JUN-2000; 2000GB-00015308
06-OCT-2000; 2000GB-00024544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.00,
                                                                                                                                                                                                                                                                                           (CELL-) CELLTECH PHARM LTD.
                                                                                                                                                                                                                                                                                                                                     Pumpens P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                 .639
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P-PSDB; AAE17018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                     Li J,
                                                                                                   WO200198333-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-2002
                                                                                                                                          27-DEC-2001
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Gaps

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Indels

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RESULT 11

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AAD31509/

Key

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DB 6; Length 639;

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                                                                                Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                               DB 4; Length 655;
                                                                                                                                                                     Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;
                             ŝ
                             De Gendt
                                                                         Claim 3; Fig 7; 94pp; English.
     99EP-00870252.
                   (INNO-) INNOGENETICS NV.
                             Stuyver L, Van Geyt C,
                                       WPI; 2001-374785/39.
    03-DEC-1999;
07-DEC-1999;
                                                                                                                                                                               Query Match
                                                               therapy
$XXCCCCCCCCCCX8XXIIIIXXBXBXBXXBX
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ö,
                      Gaps
                      ;
                      0; Indels
100.0%; Score 20; DI
80.0%; Pred. No. 13;
                    4; Mismatches
          Local Similarity 80.0
                     Matches
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43 GACATGAACAAGAGATGATT 24 1 GACAUGAACAAGAGAUGAUU 20 ð 셤

AAH77568 standard; DNA; 655 AAH77568;

BP

19-OCT-2001 (first entry)

HBV genotype G strain FR2 preCore/Core DNA.

Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol; HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg; HBeAg; ds. HBeAg;

Hepatitis B virus.

WO200140279-A2

07-JUN-2001

20-NOV-2000; 2000WO-EP011526.

99EP-00870252 99US-0169287P 03-DEC-1999; 07-DEC-1999;

(INNO-) INNOGENETICS NV

De Gendt S; Van Geyt C, Stuyver L,

WPI; 2001-374785/39

Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and therapy

Claim 3; Fig 7; 94pp; English.

Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

Gaps .; 0 DB 4; Length 655; Indels .; 0 4; Mismatches 13; 100.0%; Score 20; Pred. No. 80.08; Local Similarity 80.0 les 16; Conservative Query Match Best Loca Matches

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1 GACAUGAACAAGAGAUGAUU 20 ||||:|||||||||||:: 43 GACATGAACAAGAGATGATT 24

AAH77574/c RESULT 14

AAH77574 standard; DNA; 655

AAH77574;

(first entry) 19-OCT-2001 HBV genotype G strain US10 preCore/Core DNA.

Hepatitis B virus; HBV; preCore; Core; preSl; preS2; HBS; HBX; HBPol; HBsAq; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg; HBeAg; ds.

Hepatitis B virus.

WO200140279-A2

07-JUN-2001.

20-NOV-2000; 2000WO-EP011526.

99EP-00870252. 99US-0169287P 03-DEC-1999; 07-DEC-1999;

(INNO-) INNOGENETICS NV

De Gendt ς, Stuyver L, Van Geyt

WPI; 2001-374785/39.

Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and

```
human hepatitis B virus (HBV) genotype, provisionally named genotype G.
This genotype was found with a high prevalence in patients chronically
infected with HBV and residing in Europe and the USA. The invention
relates to a fully defined sequence of 3248 nucleotides as given in
sequence that is degenerate to the mentioned sequence, or
sequence that is degenerate to the mentioned sequences. These
colorable is degenerate to the mentioned sequence in a biological
sequence that is degenerate to the mentioned sequence with sequence, or
colorable is degenerate to the mentioned sequence of
colorable is degenerate to the proteins and proteins encoded by
the polynucleotides are useful for detecting antibodies in a biological
sample. Ligands that bind to the proteins and antibodies directed against
the proteins are useful for detecting the proteins and for detecting
the proteins are useful for detecting the proteins and for detecting
the proteins are useful for detecting the proteins and so useful for
consistent and HBEAAG (precore precursor proteins). They are also useful for
present sequence is provided in an alignment of preCore/Core sequences of
an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FRZ, USI, US3,
colorable in the protein and the p
                                                                                                                                                             invention relates to the complete nucleic acid sequence of a new
                                                          Claim 3; Fig 7; 94pp; English
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DB 4; Length 655; Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other; 0; Indels 4; Mismatches 100.0%; Score 20; DI 80.0%; Pred. No. 13; 1 GACAUGAACAAGAGAUGAUU 20 16; Conservative Local Similarity Query Match Best Local S Matches ò

43 GACATGAACAAGAGATGATT 24 ద

7573/c AAH77573 standard; DNA; 655 BP. AAH77573;

HBV genotype G strain US7 preCore/Core DNA. (first entry) 19-OCT-2001

Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol; HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg; HBeAg;

Hepatitis B virus.

WO200140279-A2

07-JUN-2001

20-NOV-2000; 2000WO-EP011526.

99EP-00870252. 03-DEC-1999; 07-DEC-1999;

(INNO-) INNOGENETICS NV

Gendt <u>S</u> ú Van Geyt Stuyver L,

WPI; 2001-374785/39

Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and therapy

Claim 3; Fig 7; 94pp; English.

The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the USA. The invention

specification, as sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for the genetyping. The proteins encoded by the polynucleotides are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins and antibodies directed against the proteins are useful for detecting the proteins and for detecting HBCAG and HBCAG precents proteins. They are also useful for preparing a vaccine or medicament for treating HBV infections. The an HBV genotype A strain (HBVACPS) and 7 strains (FRI, FR2, USI, US3, US1, US3, US1, US3, US1, US3, relates to a fully defined sequence of 3248 nucleotides as given in 8866666666668888

Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

Gaps ö DB 4; Length 655; 0; Indels Score 20; DB Pred. No. 13; 4; Mismatches 4. 100.001 80.08; Query Match
Best Local Similarity 80.0'
Matches 16; Conservative

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Search completed: March 17, 2005, 06:48:42 Job time : 172.333 secs

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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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March 17, 2005, 05:44:58; Search time 1386.27 Seconds (without alignments) 549.162 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-08-901-612A-61 20

1 gacaugaacaagagaugauu 20 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

34239544 segs, 19032134700 residues Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

9b_est1:*
9b_est2:*
9b_est3:*
9b_est4:*
9b_est6:*
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9b_est6:* EST: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | | | | | | | | | | | • | | | | | | | | | | | | | |
|-----------|--------------------------|-----------|----------|-----------|----------|-----------|-----------|-----------|----------|-----------|----------|----------|-----------|----------|-----------|----------|-----------|----------|-----------|-----------|----------|----------|----------|----------|-----------|
| | ion | OG1BK24TH | _ | OG1CZ28TH | _ | Arabidops | KS11017B1 | A0504F09- | BX837806 | HS 3140 B | _ | | Mus muscu | | EST0117 T | | rswjb0_00 | | 601283896 | CH240 13N | | | | _ | 602084906 |
| | Description | CG381974 | CG381984 | CG373212 | CG373225 | BX288914 | CA520799 | CF906991 | BX837806 | AQ183243 | CN958899 | AZ654527 | AK015232 | AQ961278 | CF198522 | CF909462 | CK517114 | BH366000 | BE388774 | BZ898091 | CE163565 | C0817689 | AQ961277 | CL809904 | BF678287 |
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| ES | | ! | | | | | ٠ | ٠. | | | | | | | | | | | | | | | | | |
| SUMMARIES | | CG381974 | CG381984 | 3333212 | CG373225 | BX288914 | CA520799 | CF906991 | BX837806 | AQ183243 | CN958899 | AZ654527 | AK015232 | AQ961278 | CF198522 | CF909462 | CK517114 | BH366000 | BE388774 | BZ898091 | CE163565 | 00817689 | AQ961277 | CL809904 | BF678287 |
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| | DB | 6 | 0 | σ | σ | 9 | 9 | 7 | 2 | æ | 7 | œ | ٣ | œ | 7 | 7 | 7 | æ | 7 | æ | 0 | 7 | œ | σ | 7 |
| | Query Match Length DB | 763 | 773 | 846 | 892 | 280 | 305 | 313 | 423 | 426 | 442 | 450 | 509 | 527 | 570 | 574 | 919 | 628 | 631 | 652 | 682 | 683 | 721 | 794 | 821 |
| æ | Query Match | 92.0 | 92.0 | 92.0 | 92.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 87.0 |
| | Score | 18.4 | 18.4 | 18.4 | 18.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 |
| | ReBult No. | 1 | 2 | m | 4 | Ŋ | y | 7 | œ | δ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 |
| | Re | • | υ | U | | U | | U | | U | | | | O | | U | | υ | | υ | | Ü | | O | |
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| _ | | | CC068329 CSU-K33r. | | | | BI378081 BFLG3 001 | | | | | CL543431 OB Ba006 | | | | | BG733602 Cs-20d Ci | | | BZ385056 SALK_1363 |
|----------|----------|----------|--------------------|----------|----------|----------|--------------------|----------|----------|----------|----------|-------------------|----------|----------|----------|----------|--------------------|----------|----------|--------------------|
| CC090167 | CC131380 | BF541940 | CC068329 | CNSOA5V5 | AW760013 | AL819446 | BI378081 | AG140746 | BX114353 | CC786410 | CO368799 | CL543431 | CNS06RAQ | BI127956 | BI128183 | BG125265 | BG733602 | BE428564 | BI473621 | BZ385056 |
| œ | æ | N | æ | m | ~ | Н | 4 | σ | Ŋ | σ | 7 | σ | σ | 4 | 4 | 4 | 4 | ~ | 4 | 8 |
| 859 | 870 | 885 | 903 | 1340 | 472 | 532 | 577 | 687 | 730 | 768 | 778 | 808 | 1013 | 124 | 170 | 195 | 195 | 218 | 234 | 251 |
| 87.0 | 87.0 | 87.0 | 87.0 | 87.0 | 85.0 | 85.0 | 85.0 | 85.0 | 85.0 | 85.0 | 85.0 | 85.0 | 85.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 |
| 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17 | 17 | 17 | 17 | 17 | 17 | 17 | 17 | 17 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 |
| 25 | 56 | 27 | 28 | 59 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
| υ | | υ | υ | | | υ | υ | | | υ | | | | | | | | υ | υ | |
| | | | | | | | | | | | | | | | | | | | | |

ALIGNMENTS

| RESULT 1 CG381974 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM | CG381974 763 bp DNA linear GSS 26-AUG-2003 GG1BK24TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0724C23, genomic survey sequence. CG381974.1 G1:34299241 CGSS. Zea mays Zea mays Zea mays Zea mays Zea mays |
|---|---|
| REFERENCE AUTHORS | Burstyces, VIIIangeriaes, Streptopurca; Bunitypurca; Inacineopurca; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 763) Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. |
| TITLE JOURNAL COMMENT | Consortium for Maize Genomics Unpublished (2002) Other_GSSs: OGIBK24TV Contact: Cathy Whitelaw |
| FEATURES | 912 Medical Center Drive, Rockville, MD 20850, USA Tal: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TR Class: sheared ends. Location/Qualifiers 1. 763 / organism="Zea mays" /mol_type="genomic DNA" / farain="BT3" / clone="ZMMBMA0724C23" / clone ="ZMMBMA0724C23" / clone ="ZMMBMA0724C23" / clone ="ZMMBMA0724C23" / clone ="Locker = TAMBMA0724C23" / clone = TAMBMA0724C23" |
| ORIGIN | |
| Query Match Best Local Matches | Query Match 92.0%; Score 18.4; DB 9; Length 763; Best Local Similarity 75.0%; Pred. No. 4.2e+02; Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0; |
| Oy Op | 1 GACAUGAACAAGAGAUGAUU 20 : : 572 GGCATGAACAAGAGATGATT 591 |

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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

TITLE JOURNAL COMMENT

FEATURES

RESULT 2 CG381984/c

LOCUS DEFINITION

ACCESSION

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CG373225
OGICZ28TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0734E08,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae; Zea.

1 (bases 1 to 892)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, M., Fandiman, M.A., Bedell, J.A., Robling, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Unpublished (2002)
Other GSS: OG10228TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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/note="vector: pBGSK-; Site 1: HincII; 0.7-1.5 kb
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methylation filtered genomic DNA library"
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9712 Medical Center Drive, Rockville, MD 20850, USA Fat: 301-888-5643
Fax: 301-888-5643
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
92.0%; Score 18.4; DB 9;
Best Local Similarity 75.0%; Pred. No. 4.38+02;
Matches 15; Conservative 4; Mismatches 1;
                                                                                                                                                                                                              /mol_type="genomic DNA"
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/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db xref="taxon:4577"
                                                                                                                                                                                      organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
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1..892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540 GGCATGAACAAGAGATGATT 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACAUGAACAAGAGAUGAUU 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG373225
CG373225.1 GI:34290492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: sheared ends.
                                                                                                                                                                1. .846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
Zea mays
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                                                                                                                                                                     Source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
CG373225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
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                                                            773 bp DNA linear GSS 26-AUG-2003 OG1BK24TV ZM 0.7 1.5 KB Zea mays genomic clone ZMWBMa0724C23, genomic survey sequence.
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                                                                                                                                                                                                                                                                 Leasuryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Unpublished (2002)
Other_GSS: OGIBK24TH
Contact: Cathy Whitelaw
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citck,R.W., Numberg,A., Robbins,D. and Lakey,N.
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/mol type="genomic DNA"
/db_xref="taxon:4577"
/clone="zMabMa0724C23"
/clone="lib="zM 0.7 1.5 KB"
/note="Vector: pBcSk-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Rockville, MD 20850, USA
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                   CG381984.1 GI:34299251
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Contact: Cathy Whitelaw
TIGR
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Query Match

RESULT 3 CG373212/c

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TITLE JOURNAL

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15; Conservative
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Direct Submission

L. Submitter (11-Wahz-2004) Weisshaar B., Max-Planck-Institut fuer

Burdetted (11-Wahz-2004) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion within the locus defined by BAC clone

13423. Details on the protocols used for generation of the sequence

are described in References 1-3. The sequences are generated at the

MPI for Plant Breeding Research in the context of the GABI-Kat

project. GABI-Kat is part of the German Plant Genomics program

designated (GABI'. Information on line availability can be found

at: http://www.mpiz-koeln.mgs.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC16 I (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed.
                                                                                                           вьдевуде GSS 02-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-421D09-018141,
                                                                                                                                                                                                                                                                                     Eukaryofa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/clone="GK-421D09-018141"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                             Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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/mol type="genomic DNA"
/strain="Columbia 0"
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22755829
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3; Mismatches

15; Conservative

Best Local Similarity

Matches

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (Dases I to 313) Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H. Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                              EST 15-NOV-2002
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
asterids, lamids, Solanales, Solanaceae; Capsicum.
1 (bases 1 to 305)
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S.,
Hur, C.-G. and Choi, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Research Center and National Center for Genome Information Korea Research Institute of Bioscience and Biotechnology P.O. Box 115, Yusong, Taejeon, 305-600, Republic of Korea Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doli@mail.kribb.re.kr
Plate: 017 row: B column: 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen Unpublished (2001)
Contact: Doil Choi
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Mus musculus cDNA clone NIA:A0504F09 IMAGE:30743204 5', mRNA
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    .305
    /organism="Capsicum annuum"

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/db_xref="taxon:4072"
/clone_lib="KS11"
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Juckes 1. Sall; Juckes 2. Not1; Mouse cDNA project by the Laboratory of Genetices. Not1; Mouse cDNA project by the Laboratory of Genetices. National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 153-1558 (2001). [PMID: 11544199]). Total RNAS were obtained from Dr. Akihiro Umczawa (Keio University School of Medicine, Japan). Double stranded CDNAS were synthesized with an Oligo (dT) primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX837806
BX837806 Arabidopsis thaliana Hormone Treated Callus Col-0
Arabidopsis thaliana clone GSLTPGH21ZC04 5PRIM, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                 /clone="NIA:A0504F09 IMAGE:30743204"
/dev stage="9-15C cells"
/lab_host="DH10B"
/clone lib="NIA Mouse Mesenchymal Stem Cell CDNA Library
(Long I)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots,
rosids; eurosids II, Brassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
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                                                                                                                                                                                                                                   mol_type="mRNA"
strain="C3H/He mice"
db_xref="niaEST:A0504F09-5"
db_xref="taxon:10090"
                                                                                                                                                                                                               'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
                                                                                           Seg primer: M13 Reverse
High quality sequence stop: 313
POLYA=No.
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Matches 15; Conserv
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BX837806
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: :www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV IRRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences).
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
Location of the June 2003 version of EF/EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.
11 (base1 to 426)
Mahairas,G.C., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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/clone_lib="Arabidopsis thaliana Hormone Treated Callus
Col-0"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

    423
/organism="Arabidopsis thaliana"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="GSLTPGH21ZC04"
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Location/Qualifiers
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Class: BAC ends
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/ecotype="Col-0"
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403 ACATGAAGAAGAGATGATT 421
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Unpublished (2004)
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Matches 14; Conservative
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(http://www.iax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gol electrophoreais. Vector DNA was prepared from a derivative of pWD42 (gi|473214|qb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                           SM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 450)
Bunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Railly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von
Niederhausern,B. Weiss
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Dm. 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Wector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK015232
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930429C20 product:unclassifiable, full insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0528 row: D column: 16
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: plasmid ends
High quality sequence stop: 450.
Location/Qualifiers
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/clone="UUGC1M0528D16"
                                                                              Mus musculus (house mouse)
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132 GAAATGAACAAGAGATGAT 150
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Fax: 801 585 7177
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AZ654527.1
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AK015232
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Fundulus heteroclitus

Fundulus heteroclitus

Fundulus heteroclitus

Fundulus heteroclitus

Fundulus heteroclitus

Fundulus heteroclitus

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Actinopterygii; Neopterygii; Percomorpha; Atherinomorpha;

Cyprinodoniiformes; Fundulidae; Fundulus.

Cyprinodoniiformes; Fundulidae; Fundulus.

E 1 (bases 1 to 442)

Roach, J.L. and Whitehead, J.A.

Fundulus Functional Genomics: EST Database for Teleost Fish

Contact: Crawford iab

Marine Genomics - Crawford iab

Rosenstiel School of Marine and Atmospheric Science - University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CN958899 442 bp mRNA linear EST 08-JUN-2004 6399_100122_44 Fundulus Heteroclitus Liver Fundulus heteroclitus cDNA, mRNA sequence.
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1M0528D16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0528D16 R, genomic survey sequence.
                                                                                                                                                    /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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Database Web Interface
http://genomics.rsmas.miami.edu/funnybase/super_craw3/
Plate: 100122 row: E column: 6.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.0%; Score 17.4; DB 7; Length 442; 78.9%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                        Length 426;
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                                                                                                                                                                                                                                                                                                                                      1; Indels
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/clone lib="Fundulus Heteroclitus Liver"
/note="Organ: Liver"
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Pred. No. 1.2e+03;
                                                                                                      /clone="Plate=3140 Col=4 Row=D"
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                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:8078"
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CN958899.1 GI:48440488
                                                                                                                                                                                                                                                                                   Query Match 87.0%;
Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                                                                 /sex="male"
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Unpublished (2000)
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AQ961278
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

In Nature 420, 563-573 (2002)

Adachi, J. Aizawa, K. Akahira, S. Akimura, T. Arai, A. Aono, H.,

Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,

Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,

Hiraoka, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M.,

Kasukawa, T., Kato, H., Kavai, J., Kojima, Y., Konno, H., Kouda, M.,

Kasukawa, T., Sato, R., Sakai, C., Sakai, Y., Okido, T., Owa, C.,

Saito, R., Sakai, C., Sakai, Y., Sano, H., Sagaki, D.,

Saito, R., Sakai, C., Sakai, T., Sano, H., Sagaki, D.,

Saito, R., Sakai, C., Sakai, Y., Shiraki, T., Sogabe, Y.,

Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,

Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,

Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

L. Submitted (10-UUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Gences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail:genome-resease.riken.jp,

URL:http://genome.genc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Gomem Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Murametsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer General Connec Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.gsc.riken.jp/) for further
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium and the RIKEN Genome Exploration Research
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                        AK015232.1 GI:12853489
HTC; CAP trapper.
Mus musculus (house mouse)
                                                                                                                     Mus musculus
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/tissue_type="testis"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
1. .509
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 527)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Felblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana.and identification of sequence-based
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/note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bmail: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Seg primer: TR
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.0%; Score 17.4; DB 3; 73.7%; Pred. No. 1.2e+03; live 4; Mismatches 1;
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/db_xref="taxon:10090"
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/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="unclassifiable"
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Laboratory of Genetics
National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Bmail: cdna@lgsun.grc.nia.nih.gov
Plate: A0536 row: H column: 03
Seg primer: M13 Reverse
High quality sequence stop: 574
POLYANNO:
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                                        Contact: Dawood B. Dudekula
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Matches 15; Conservative
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Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Caryophyllales; Tamaricaceae; Tamarix.

(bases 1 to 570)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 574)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang, Y., Yang, C., Jiang, J., Liu, G., Wu, J. and Liu, Z.
EST aquired from cDNA library of Tamarix androssowii treated with
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                                                                                                                                                                                                                                                                                     CF198522 570 bp mRNA linear EST 01-AUG-:
EST0117 Tamarix androssowii leaf Tamarix androssowii CDNA, mRNA
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                                                           Length 527;
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Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yucheng Wang
Forestry Source and Environment College
Northeast Forestry University
Hexing 26, Harbin, Heilongjiang, 150040, P.R. China
Tel: 086-451-2190607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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  sheared to 0.9-1 Kbp before ligation."
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/db_xref="taxon:189785"
/fisuue type="leaf"
/clone_lib="Tamarix androssowii leaf"
                                                         Score 17.4; DB 8;
Pred. No. 1.2e+03;
3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: WANGYUCHENG1029@YAHOO.COM.CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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                                                                                                                                                                   160 ACATGAACAAGAGAAGATT 142
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143 ACATGAACAAGAGGTGATT 161
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73.7%;
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                                                    Query Match
Best Local Similarity 78.9°
Matches 15; Conservative
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2.2 ug of total RNA, treated with T4 DNA polymerse, and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/Chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/Chloroform and Centricon 100. The CDNAs were digested with Sal1 and Not1 enzymes and cloned into Sal1/Not1 site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Site_2: Not1; Mouse cDNA project by the Laboratory of Genefice, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgaun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001), [PMID: 11544199]). Total RNAs were obtained from Dr. Akihiro Umezawa (Keio University School of Medicine, Japan). Double-stranded cDNAs were synthesized with an Oligo(dT) primer
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                                                                                                             /mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="NYA:A0536H03 IMAGE:30746294"
/dev_stage="9-15C cells"
/lab_host="DH108"
                                                                          /organism="Mus musculus"
Location/Qualifiers
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Run on:

Sequence:

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AY274428 HEPATILIS
AY274429 HEPATILIS
AY274431 HEPATILIS
AY274431 HEPATILIS
AY274432 HEPATILIS
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AY382501 HEPATILIS
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AY38251 HEPATILIS
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AY38
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Unclassified.
1 (Dass 1 to 20)
1 (Dass 1 to 20)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and Mills, J.S.
Oligonucleotides specific for hepatitis B virus
Patent: US 5856459-A 15 05-JAN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
Unclassified.
1 (bases 1 to 30)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
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Pred. No. 14;
3; Mismatches 0
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    .20
    /organism="unknown"
    /mol_type="unassigned DNA"

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Sequence 15 from patent US 5856459.
AR027817
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Sequence 40 from patent US 5856459.
AR027842
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AY382525
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 Similarity
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Best Local S:
Matches 17
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AR027843 Sequence
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AY32559 Hepatitis
AY32551 Hepatitis
AY325573 Hepatitis
AY325573 Hepatitis
AY325591 Hepatitis
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AY325591 Hepatitis
AR136703 Hepatitis
AB16703 Hepatitis
AB16703 Hepatitis
AB16703 Hepatitis
AB16731 Hepatitis
AB16731 Hepatitis
AR154503 Hepatitis
AY254503 Hepatitis
AY274419 Hepatitis
                                                                                                                        March 17, 2005, 04:07:57; Search time 683.733 Seconds (without alignments) 1417.372 Million cell updates/sec
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                             4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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Minimum DB Maximum DB

Database

Result

8

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Searched:

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Gaps

source

ORIGIN

FEATURES

TITLE JOURNAL

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Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses; Hepadnaviridae, Orthohepadnavirus.

1 (bases 1 to 174)
Feitelson,M.A., Duan,L.X., Guo,J. and Blumberg,B.S.
Feitelson,M.B. mutants associated with surface antigen-positive hepatitis B virus infections
Gastroenterology 108 (6), 1810-1819 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus isolate A611252E X protein gene, partial cds, and A7329529
                                                                                                                 S77749
preC {X/preC region, deletion mutant} [hepatitis B virus HBV, host=human, serum, patient 5 isolate, Genomic DNA Mutant, 174 nt].
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Submitted (23-JUN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (Dases 1 to 253)
Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., Silva,L.C. and Carrilho,F.J.
Silva,L.C. and Carrilho,F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 165980] from the original journal article. Location/Qualifiers
1. 174
/organism="Hepatitis B virus"
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Rebello Pinho,J.R., Sitnik,R., Carrilho,F.J., Da Silva,L.C. and
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/mol_type="genomic DNA"
/isolate="A611252E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="preC"
/note="no start codon found"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 20; DB Best Local Similarity 85.0%; Pred. No. 16; Matches 17; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:10407"
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   1 TAAGGGTCGAUGUCCAUGCC 20
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Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
Mills, J.S.
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               Oligonuclectides specific for hepatitis B virus Patent: US 5856459-A 40 05-JAN-1999;
Location/Qualifiers
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Patent: US 5856459-A 41 05-JAN-1999;
Location/Qualifiers
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85.0%; Pred. No. 14;
:ive 3; Mismatches
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                                                                                                             /mol_type="unassigned DNA"
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Carmichael,E.
Antiviral poly-and oligonucleotides
Patent: US 5728518-A 9 17-MAR-1998;
Location/Qualifiers
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Sequence 9 from patent US 5728518.
192348.
192348.1 GI:3936818
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Heparitis B virus isolate D604917E X protein gene, partial cds; and Ay329573
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Hepatitis B virus isolate D296668B X protein gene, partial cds; and
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 253)
Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., I Silva, E.C. and Carrilho,F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
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Rebello Pinho, J.R., Sitnik, R., Carrilho, F.J., Da Silva, L.C. and
Bernardini, A.P.
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/mol type="genomic DNA"
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Best Local Similarity 85.0%; Pred. No. 17;
Matches 17; Conservative 3; Mismatches
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Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

1 (bases 1 to 253)
Sitnik, R., Rebello Pinho, J.R., Bertolini, D.A., Bernardini, A.P., Sitnak, R., Rebello Pinho, F.J.

Silva, L.C. and Carrilho, F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in
Brazilian Patients
J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
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Rebello Pinho,J.R., Sitnik,R., Carrilho,F.J., Da Silva,L.C. and
Bernardini,A.P.
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                                                                                                                                                                                                                                                                                                                                                                                             /product="X protein"
|Protein | d="AAQ95940.1"
|db_xref="GI:37625497"
|/translation="STTDLEAYFKDCLFKDWBELGEEIRLKVPVLGGCRHKLVCAPAS
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Viruses; Ratroid viruses; Hepadnaviridae; Orthohepadnavirus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
Viruses: Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
Saltnik, R., Rebello Pinho, J.R., Bertolini, D.A., Bernardini, A.P., Da Silva, L.C. and Carrilho, F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
                    Da
                                                                                                                                                                          Direct Submission
Submitted (23-JUM-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
Location/Qualifiers
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Submitted (23-JUN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
              Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., Silva,L.C. and Carrilho,F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
                                                                                                                                      Rebello Pinho, J.R., Sitnik, R., Carrilho, F.J., Da Silva, L.C. and
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Rebello Pinho, J.R., Sitnik, R., Carrilho, F.J., Da Silva, L.C. and
Bernardini, A.P.
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/protein id="AAQ95949.1"
/db_xref="GI:37625448"
/translation="MQLFHLCLISCSCPTVQASKLCLGWL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
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                                                                                                                                                                                                                                                                                   /organism="Hepatitis B virus"
/mol type="genomic DNA"
/isolate="D604917E"
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/organism="Hepatitis B virus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 17;
3; Mismatches
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/codon_start=3
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Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                         (bases 1 to 253)
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                                                                                                                                                             Bernardini, A. P
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DEFINITION
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                  AUTHORS
                                                                                    JOURNAL
                                                                                                        PUBMED
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Hepatitis B virus
Hepatitis B virus
Viruses; Betroid viruses; Hepadnaviridae; Orthohepadnavirus.

(Loases 1 to 294)
Castro,L.D., Niel,C. and Gomes,S.A.
Low frequency of mutations in the core promoter and precore regions of hepatitis B virus in anti-HBe positive Brazilian carriers
BMC Microbiol. 1 (1), 10 (2001)
                                                                                     /translation="STTDLEAYFKDCLFKDWEELGEELRLLIFVLGGCRHKLVCAPAP
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95. .>294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           akyy0000 294 bp DNA linear VRL 06-MAN Hepatitis B virus isolate D3 X protein gene, partial cds; and nonfunctional precore/core protein gene, partial sequence.
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                                                                                                                                                                                                                                              translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
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/mol type="genomic DNA"
isolate="D3"
                                                                                                                                                                                                                                                                                                               DB
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De Castro,L., Niel,C. and Gomes,S.A.
Direct Submission
                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DE
85.0%; Pred. No. 17;
:ive 3; Mismatches
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85.0%; Pred. No. 17;
ive 3; Mismatches
                                                                                                                                                      /codon_start=1
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/db_xref="GI:37625471"
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As anaka Y. and Mizokami, M.

Ranaka Y. and Mizokami, M.

Direct Submission

AL Submission

AL Submitted (15-MAR-2004) Yasuhito Tanaka, Nagoya City University

Graduate School of Medical Sciences, Department of Clinical

Molecular Informative Medicine; I Kawasumi, Mizuho-cho, Mizuho-ku,

Nagoya, Aichi 467-8601, Japan (E-mail:ytanaka@med.nagoya-cu.ac.jp,

Tel:81-52-853-8292, Fax:81-52-842-0021)

RS Location/Qualifiers

1. 398

/ organism="Hepatitis B virus"

/ mol type="genomic DNA"

/ db_xref="taxon:10407"

/ clone="NBP75"

/ lone="NBP75"

/ note="precore-core region"

/ note="precore-core region"
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LSFLPSDFFPSVRDLLDTASALYRBAL"
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Tanaka,Y. and Mizokami,M.

Direct Submission

Submitted (15-MAR-2004) Yasuhito Tanaka, Nagoya City University

Graduate School of Medical Sciences, Department of Clinical

Molecular Informative Medicine; 1 Kawasumi, Mizuho-cho, Mizuho-ku,

Nagoya, Aichi 467-8601, Japan (E-mail:ytanaka@med.nagoya-cu.ac.jp,

Tel:81-52-853-8252, Fax:81-52-842-0021)

Location/Qualifiers
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AB167637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/mol_type="genomic DNA"
/db xref="taxon:10407"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184. >398
/note="precore-core region"
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85.0%; Pred. No. 18;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          /product="polyprotein"
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AB167637/c
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ACCESSION
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                                                                                                                                                                                                                                                        Tong, S.P., Li, J.S., Vitvitski, L. and Trepo, C. Active hepatitis B virus replication in the presence of anti-HBe is associated with viral variants containing an inactive pre-C region Virology 176 (2), 596-603 (1990)
                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 333)
Li,J.S., Tong,S.P., Wen,Y.M., Vitvitski,L., Zhang,Q. and Trepo,C.
Hepatitis B virus genotype A rarely circulates as an HBe-minus
mutant: possible contribution of a single nucleotide in the precore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /proteIn_id="AaB03102.1"
/db_xref="G1:306268"
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PEHCSHHHTALRQAILCWGBLWTLATWVGANLDDPASR"
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Hopatitis B virus gene for polyprotein, partial cds, clone: NEP75.
                                                 HPBHBED 333 bp DNA linear VRL 28-JUN-1996 Hepatitis B virus precore and core protein gene, 5' end of cds.
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Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10407"
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/product="precore protein"
82. .84
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J. Virol. 67 (9), 5402-5410 (1993)
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S Hasegawa, I., Tanaka, Y. and Mizokami, M.
Direct Submission

Lorect Submission

Solence, 1 Kawasumi, Mizuho-ku, Nagoya City University
Graduate School, Department of Internal Medicine and Molecular
Science, 1 Kawasumi, Mizuho-cho, Mizuho-ku, Nagoya, Aichi 467-8601,
Japan (E-mail:izu-hase@med.nagoya-cu.ac.jp, Tel:81-52-853-8216,
Pax:81-52-852-0849)

Location/Qualifiers

Location/Qualifiers

| Amol type="genomic DNA"
| foolar fee="genomic DNA"
| foolar fee="
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Hepatitis B virus X, preC/C genes for polyproteins, isolate:
SAF662.
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                                           Gaps
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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                                               0; Indels
Best Local Similarity 85.0%; Pred. No. 18; Matches 17; Conservative 3; Mismatches
                                                                                                                                                     287 TAAGGGTCGATGTCCATGCC 268
                                                                                                          1 TAAGGGTCGAUGUCCAUGCC 20
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AB163815.1 GI:49387444
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/gene="prec/C"
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Matches 17; Conservative 3; Mismatches 0; Indels

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Search completed: March 17, 2005, 08:14:17

Aad31765 Hepatitis
Aad61842 Hepatitis
Aad60866 Hepatitis
Aad60866 Hepatitis
Aad60810 Plasmid p
Aas16094 HBV viral
Aas16094 HBV viral
Ad94544 SDMCore d
Ad789273 Lab-on-ch
Ad789266 Lab-on-ch
Aad78913 HBV ampli
Aad78913 HBV ampli
Aad78913 HBV Liha2
Ad46961 PCR prime
Adm83206 PCR prime
Abk674212 B cell ep
Abk6743 Primer fo
Ade80023 Primer fo
Ad680023 Primer fo
Ad680023 Chimeric
Ad646965 PCR prime
Ad86065 PCR prime

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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The present sequence represents a synthetic oligonucleotide HBV92b which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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/note= "Internucleotide linkages are phosphorothioate"
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AAS16094
AAS16092
AAS16093
ADS9254
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AAQ45813
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Roberts NA, Roberts PC, Slade A;
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Aar72619 Heparitis
Aar72620 Heparitis
Aar72621 Heparitis
Aar72631 Heparitis
Adc64743 Heparitis
Add37422 Heparitis
Aad31509 Heparitis
Aad31709 Heparitis
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Aav82686 Fulminant
Aav82689 Fulminant
Aav82689 Fulminant
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                                                          March 17, 2005, 04:03:33; Search time 171.333 Seconds (without alignments) 691.020 Million cell updates/sec
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         GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AAT72619
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ADC64743
AAD21422
AAD31509
AAA71734
AD007220
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The present sequence represents a synthetic oligonucleotide HBV92Mb which its complementary to a portion of the hepatitis B virus (HBV) RMJ. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non-contiguous regions of an HBV uncleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
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2.5;
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Roberts NA, Roberts PC, Slade
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/mod_base= gm
     96WO-EP002432
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Matches 20; Conservative
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sample. The antisense oligonucleotide, and oligonucleotides containing a
              sequence which is complementary to at least two non-contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
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                                                                                                  Query Match
Best Local Similarity 85.0%; Pred. No. 2.5;
Matches 17; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus RNA antisense oligonucleotide HBV92Mb
                                                                        Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
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mod_base= OTHER
note= "2'-0-methyladenosine"
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The present sequence represents a synthetic oligonucleotide HBV-91b which contains a sequence which is complementary to at least two non-contiguous regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
          The present sequence represents a synthetic oligonucleotide HBV-90Mb which contains a sequence which is complementary to at least two noncontiguous regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
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    /*tag= a
    /note= "Internucleotide linkages are phosphorothioate"

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         sequence represents a synthetic oligonucleotide HBV-90Mb
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100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 85.0%; Pred. No. 2.6;
Matches 17; Conservative 3; Mismatches 0; Indels
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Pred. No. 2.6;
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           note = "2'-0-methyladenosine"
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note= "2'-OMe RNA"
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mod_base= OTHER
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Claim 5; Page 15; 81pp; English

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The present sequence represents a synthetic oligonucleotide HBV-91Mb which contains a sequence which is complementary to at least two noncontiguous regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
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note= "Internucleotide linkages are phosphorothioate"
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Hepatitis B virus RNA antisense oligonucleotide HBV-91Mb.
                         HBV; HBV infection; inhibition; replication; ss
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/note= "2'-0-methyladenosine"
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/note= "2'-OMe RNA"
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PC, Slade A;
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3; Mismatches
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          TAAGGGTCGAUGUCCAUGCC 20
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les 17; Conservative
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(first entry)

04-SEP-1997

AAT72621;

AAT72621 ID AAT XX AC AAT XX DT 04-(

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Hepatitis B virus (HBV) core antigen (HBcAg) encoding DNA #1.
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                                                                                                                                                                                                                                                                                                                                                                                                Screening of antiviral agents by protein-priming activity of hepatitis B virus DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method of screening for an antiviral agent by the protein-priming activity of hepatitis B virus (HBV) DNA polymerase. Also described is developing an antiviral agent with a high selectivity to HBV which can be used for high-throughput screening. The present sequence represents an RNA oligonucleotide which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                              Gaps
                                                                                                                                                                                                            screening; antiviral; hepatitis B virus; HBV; DNA polymerase; ss.
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                                                                                                                                                                                         Hepatitis B virus DNA polymerase related RNA oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 20; DB 10; Length 31; 85.0%; Pred. No. 2.6; 1.1ve 3; Mismatches 0; Indels
                          Score 20; DB 2; Length 30;
Pred. No. 2.6;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 Yoon GS;
         BP; 7 A; 6 C; 11 G; 3 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31 BP; 10 A; 6 C; 8 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                 Ryu WS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                 Min MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 12; 13pp; Korean.
                                                                                                                                                                                                                                                                                                                                     (MOGA-) MOGAM BIOTECHNOLOGY INST. (VIRO-) VIROGEN CO LTD.
                                                               1 TAAGGGTCGAUGUCCAUGCC 20
                                                                                  11 TAAGGGTCGAUGUCCAUGCC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TAAGGGTCGAUGUCCAUGCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 TAAGGGTCGATGTCCATGCC 3
                          Query Match
100.0%; Some Seat Local Similarity 100.0%; Powatches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                19-JUL-2000; 2000KR-00041420
                                                                                                                                                                                                                                                                                                                    19-JUL-2000; 2000KR-00041420
                                                                                                                                  ADC64743 standard; RNA; 31
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                 Ji HJ, Jung SI, Kim YC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-309015/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                       Hepatitis B virus.
                                                                                                                                                                                                                                                           KR2002007891-A
                                                                                                                                                                      18-DEC-2003
         Sequence 30
                                                                                                                                                                                                                                                                              29-JAN-2002.
                                                                                                                                                                                                                               Synthetic
                                                                                                                                                     ADC64743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                       Matches
                                                                                                             RESULT 7
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                                                                                 요
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BP

AAD27422 standard; DNA; 639

18-APR-2002 (first entry)

AAD27422;

RESULT 8
AAD27422/c
ID AAD2
XX
AC AAD2
XX
DT 18-AX

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The invention relates to modified proteins comprising hepatitis B virus (HBV) core antigen (HBCAg) wherein one or more of the four arginine crepeats has been deleted and the protein comprising the C-terminal cysteine of HBCAg. The deleted region may be replaced by an epitope from a protein other than HBCAg, in which case the HBCAg acts as a carrier to present the epitope to the immune system. This chimeric protein or its cullic acid is useful as a vaccine or in a method of prophylactic or therapeutic vaccination of the human or animal body, particularly against the nucleic acid encoding the protein may be used in gene therapy or DNA vaccination protocols. The chimeric protein or its nucleic acid may also be used as the basis of a prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth disease, polio, herpes, rabies, acquired immunodeficiency syndrome (AIDS), dengue fever, yellow fever, malaria, tuberculosis, whooping cough, salmonellosis, typhoid, food poisoning, cucconding Hepatitis B virus core antigen (HBCAg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New proteins comprising a modified hepatitis B core antigen, useful as a vaccine in prophylactic or therapeutic vaccination of the human or animal body, particularly against hepatitis B virus infection.
                    prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes; hepatitis C virus; HCV; hilluenza; foot-and-mouth disease; diarrhoea; tuberculosis; polio; rabies; acquired immunodeficiency syndrome; AIDS; dengue fever; yellow fever; malaria; whooping cough; salmonellosis; food poisoning; meningitis; gonorrhea; antiviral; antibacterial; antiprotozoal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
B virus; HBV; core antigen; HBcAg; immune system; typhoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 38-39; 40pp; English
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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85.0%; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page M, Li J, Pumpens P;
                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-098223/13.
                                                                                                                                                                                                                                                               Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200198333-A2.
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ID AAD3
XX
AC AAD3
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HBV fusion protein comprising LHB and RGD encoding cDNA.
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                                                                                             Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAB10596
                                                                                                                                                                                                                                                                        (HILD/) HILDT E.
                                                                                                                                          WO200046376-A2.
                                                                                                                                                                                                                                      05-FEB-1999;
                                                                                                                                                                            10-AUG-2000
                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B (HB) core antigen fusion proteins, useful as vaccines for the prophylactic or therapeutic treatment of humans or animals against e.g. HB virus, viral hepatitis, hepatitis C virus, influenza, or foot-and-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HBcAg) fusion proteins and polynucleotides encoding such proteins. Sequences of the invention are useful in methods of prophylactic or therapeutic vaccination or to manufacture medicaments for prophylactic or therapeutic vaccination of the human or animal body against HBV, e.g. against wiral hepatitis. They are also useful as a prophylactic vaccine against e.g. hepatitis c vincia, influenza, polio, herpes, rabies, acquired immune deficiency syndrome (AIDS) or foot-and-mouth disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is a DNA encoding hepatitis B virus core antigen (HBCAg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to hepatitis B virus (HBV) core antigen
                                                                         Hepatitis B virus core antigen; HBcAg; prophylactic; viral hepatitis; therapeutic; vaccine; acquired immune deficiency syndrome; influenza; polio; herpes; rabies; AIDS; foot-and-mouth disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                           Hepatitis B virus core antigen (HBcAg) encoding DNA.
                                                                                                                                                                                                                                                                                        /*tag= c
/product= "Mature HBc protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rowlands D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches

    639
    *tag= a
    /product= "HBc protein"

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                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TAAGGGTCGAUGUCCAUGCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-2001; 2001WO-GB001607
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             (first entry)
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(first entry)
                                                                                                                                                                                                                                                                   88. .636
/*tag= c
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Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MEDE-) MEDEVA EURO LTD
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                                                                                                                                                                                                                                         . .87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gilbert R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-239995/29.
P-PSDB; AAE19793.
                                                                                                                                          Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                     WO200177158-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouth disease.
             18-JUN-2002
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08-JAN-2001
                                                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2001
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This invention describes a novel particle (A), comprising a protein coat with a fusion protein (FP), and, inside the coat, a nucleic acid (1) including the sequence for a virus-specific packaging signal (psi) and a structural gene. FP contains a virus protein (VP), a peptide (P) that mediates cell permeability and a heterologous cell-specific binding site (RGD). The invention also describes (1) producing (A) in which FP contains an HBV core antigen (HBCA), (P) and RGD; (3) PP; (4) DNA encoding FP; and (5) expression vector containing the DNA of (d). The products of the invention are used in gene therapy of cells and tissues, in vivo or ex vivo. This sequence encodes a (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Particle for cell-specific gene delivery, useful in gene therapy, comprises nucleic acid in protein coat that includes a fusion protein of viral protein, permeability peptide and cell-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Fusion protein, protein coat, virus-specific packaging signal; psi, virus protein, cell permeability, cell-specific binding site; LHB; large surface protein; core antigen; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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3; Mismatches
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10. .669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16a; Fig 1; 34pp; German.
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ADO07220 standard; DNA; 669 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hildt E, Hofschneider P;
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RESULT 10
AAA71734/c
ID AAA71
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XX
AC AAA71
XX
DT 06-AU
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The present sequence represents part of the genome of a fulminant
Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
The specification describes Hepatitis B virus (HBV) nucleic acid that has
a mutation (i.e. alteration from the normal nucleotide in any of the
genotypes A to F) in at least two of the enhancer I region, the negative
c genotypes A to F) in at least two of the enhancer I region, the negative
c genotypes A to F) in at least two of the enhancer I region, the negative
c genotypes A to F) in at least two of the enhancer I region, the negative
c genotypes A to F) in at least two of the enhancer I region, the negative
c gentide amino acid change to Cys or Met. The HBV variants of the
c nvention are used to detect binding interactions between host or viral
c proteins and HBV nucleic acid. Probes that hybridise to any of the
specified mutated regions are used to detect HBV-related disease,
c specified mutated regions are used combinations of the specified
c serologically fulminant infection, but also severe chronic infection or
c serologically nunsual forms of disease. Combinations of the specified
c mutations are associated with fulminant infections, probably because they
creduce the ability to bind inhibitory proteins in the host cell
                                                                                                                                                                                                                                                                                                          New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hepatitis B virus; variant; FHBV; HBV; binding interaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fulminant hepatitis B virus genotype D variant FHBV5 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 20; DB 2; Length 1334; 85.0%; Pred. No. 3.5; ive 3; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1334 BP; 288 A; 363 C; 311 G; 372 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 5, 85pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV82688 standard; DNA; 1395 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-EP002048.
                                                   98WO-EP002048
                                                                                                     97GB-00007221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 85.0 tes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HBV-related disease; ss.
                                                                                                                                                                                                                                                              WPI; 1999-009329/01.
                                                                                                                                                      (UNIU ) UNIV GLASGOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus.
                                                   08-APR-1998;
                                                                                                       09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9845421-A2.
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15-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fulminant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV82688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the DNA sequence of the hepatitis B virus core antigen (HBcAg) gene from HBV serotype ayw. A peptide comprising a HBV composed in claimed methods of the invention for modulating an immune response in a mammal. A method of inducing a systemic immune response to a peptide in a mammal comprises transmucosally administering conformation and peptide. The peptide is a macromolecular aggregate of the peptide. The macromolecular aggregate comprises at least 10 peptide subunits, may have composed a molecular weight of over 1,000 kDa, and is preferably at least 5 nm in diameter. It is resistant to digestive degradation, being stabilised in aggregate form by chemical treatment and/or by recombinant protein caggregate form by chemical treatment and/or by recombinant protein conversed from HBV surface protein, nucleocapsid protein or envelope protein. Transmucosal administration to a mammal of a macromolecular aggregate of a HBV surface protein enganders a systemic immune response in the mammal. A method of suppressing an immune response conversed in the mammal and administration and which may be stabilised by chemical treatment to protein engandering a monomolecular peptide from the induction of conversed to that is resistant to digestive degradation and which may be derived from a HBV protein. A monomolecular peptide is useful for the induction of converse conversed to a systemic immunity is undesirable, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating a systemic immune response to a peptide in a mammal comprises transmucosally administering a macromolecular aggregate of the peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fulminant hepatitis B virus, variant, FHBV, HBV, binding interaction,
HBV-related disease, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 20; DB 12; Length 669; Pred. No. 3.3; 3; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 20; Best Local Similarity 85.0%; Pred. No. 3 Matches 17; Conservative 3; Mismatch
/partial
/note= "No start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 TAAGGGTCGATGTCCATGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TAAGGGTCGAUGUCCAUGCC 20
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                                                                                                                                                                                    17-OCT-2003; 2003WO-US033178.
                                                                                                                                                                                                                                     17-OCT-2002; 2002US-0419279P
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                                                                               WO2004035007-A2
                                                                                                                                29-APR-2004
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Gaps

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(UNIU) UNIV GLASGOW

WPI; 1999-009329/01

Carman B;

Hepatitis B virus.

AAV82691;

RESULT 12

ઠે 셤 WO9845421-A2

The present sequence represents part of the genome of a fulminant the paraitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic. especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell Disclosure, Fig 5, 85pp, English

Sequence 1395 BP; 277 A; 387 C; 331 G; 398 T; 0 U; 2 Other; Query Match

100.0%; Score 20; DB 2; Length 1395; 85.0%; Pred. No. 3.5; 0; Indels 3; Mismatches 1 TAAGGGTCGAUGUCCAUGCC 20 17; Conservative Local Similarity Matches

917 TAAGGGTCGATGTCCATGCC 898

AAV82687 standard; DNA; 1400 BP AAV82687;

16-FEB-1999 (first entry)

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction; HBV-related disease; ss.

Fulminant hepatitis B virus genotype D variant FHBV4 sequence.

Hepatitis B virus.

15-OCT-1998

WO9845421-A2

98WO-EP002048 08-APR-1998; 97GB-00007221 09-APR-1997;

(UNIU) UNIV GLASGOW

Carman B;

WPI; 1999-009329/01.

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure; Fig 5; 85pp; English.

The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the

especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease,

8X3333333333338

Sequence 1400 BP; 287 A; 388 C; 332 G; 393 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 20; DB 2; Length 1400; 85.0%; Pred. No. 3.5; Indels °, Pred. No. 3.5; 3; Mismatches 82.0%; Best Local Similarity 85.0 Matches 17; Conservative Query Match

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917 TAAGGGTCGATGTCCATGCC 898 1 TAAGGGTCGAUGUCCAUGCC 20 ਨੇ

RESULT 15 AAV82692/c

AAV82692 standard; DNA; 1445 BP

AAV82692;

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Gaps

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16-FEB-1999 (first entry)

Fulminant hepatitis B virus genotype D variant FHBV13 sequence.

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction; HBV-related disease; ss.

Hepatitis B virus.

WO9845421-A2.

15-0CT-1998

98WO-EP002048 08-APR-1998;

97GB-00007221.

(UNIU) UNIV GLASGOW

Carman B;

WPI; 1999-009329/01.

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure, Fig 5, 85pp, English.

a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II core upstream regulatory sequence, basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has

Query Match 100.0%; Score 20; DB 2; Length 1445; Best Local Similarity 85.0%; Pred. No. 3.5; Matches 17; Conservative 3; Mismatches 0; Indels 0 XX SQ Sequence 1445 BP; 297 A; 406 C; 338 G; 404 T; 0 U; 0 Other;

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0; Gaps

Search completed: March 17, 2005, 06:48:43 Job time : 172.333 secs

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AG128210 Pan trog1 BH257065 CH230-283 CC099982 GR Ea25C BJ571152 BJ571152 CG284400 CGXBN55TV CG875596 CMBNESTV CC622611 OGULF56TV CL055525 CH216-81E AL110272 Homo sapi B1052244 PM2-GN037 B1052309 PM2-GN037 B1052309 PM2-GN037 CG323822 CGWKA72TV CG253822 CGWKA72TV CC716058 OGTA138TC CG25772 GGARA73TV CG35772 GGARA73TV CG35772 GGARA73TV CG35821 CGMKA72TV CG35821 CGMKA72TV CG35821 CGMKA72TV CG35821 CGMKA72TV

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HVSMEm0019017f Hordeum vulgare green seedling EST 19-OCT-2001
HVSMEm0019017f Hordeum vulgare green seedling EST library
HVSMEm0019017f, mRNA sequence.
B1954819
B1954819.1 GI:16300646
                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Boeideae; Triticeae; Hordeum.

1 (bases I to 680, T.

1 (bases I to 680, T.)

1 (bases I to 680, T.)
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/db_xref="taxon:112509"
/clone="HVSMEm0019017"
/clone="tayouther proper seedling leaf"
/lab_host="TJC121"
/clone lib="Hordeum vulgare green seedling EST library
HVCDNAQ014 (Blumeria infected) "
/note="Vector: pBlueeript SK(-); Site_1: EcoRI; Site_2:
XhoI; Morex (mla) plants were greenhouse grown in the R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Morex"
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 417
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence strart: 16
High quality sequence stop: 531.
Location/Qualifiers
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1. .686
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                                BJ571152
CG289400
CG875596
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CC716058
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Unpublished (2001)
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SOURCE
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AUTHORS
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BJ705222 BJ705222
BP569691 BP569691
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CL134160 104 418_1
BQ112668 EST598244
CG461236 PURRPP93TD
CG761335 ZMMBRD033
CL369255 RPC144_29
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                                                                             March 17, 2005, 05:44:58; Search time 1386.27 Seconds (without alignments) 549.162 Million cell updates/sec
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AI635930 t
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length
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729
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DRIGIN
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Wise lab at lowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria grammins f. sp. hordel, and leaves were harvested 24, 48 and 72 hr post-incoulation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) CDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or advence and contains an ibbrary preparation and
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ZMMBBb00002P18.r ZMMBBb Zea mays genomic clone ZMMBBb0002P18 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
( bases 1 to 576)
Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing of the maize genome
Unpublished (2003)
Contact: Rod Wing
Contact: Rod Wing
Miscons Enstitute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Far: 520 626 3967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 4; Length 686; 84.2%; Pred. No. 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/cultivar="B73"
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Seg primer: M13r
Class: BAC ends.
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1. .576
/organism="Zea mays"
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Best Local Similarity 84.2*
Matches 16; Conservative
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CC145068
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TTE00013587 Normalized large Tetrahymena thermophila cDNA, mRNA
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/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
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/db_xref="taxon:4577"
/clone="ZMMBBb0002P18"
/lab_host=="DH108"
/clone_lib="ZMMBb"
/note="Yector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Zea mays L. ssp. mays"
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                                                                                                                                                                                                                                                                                        Length 576;
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                                                                                                                                                                                                                                                                                        Score 17.4; DB 8;
Pred. No. 4.2e+02;
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Pred. No. 4.4e+02;
3; Mismatches 1;
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Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
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Location/Qualifiers
1...763
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/mol_type="genomic DNA"
/cultivar="B73"
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/clone="ZMMBBb0597N17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 AAGGTCGATGCCCATGCC 157
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CL248902.1 GI:41105456
GSS.
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84.2%;
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Matches 16; Conservative
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Class: BAC ends
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CN589115
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CL248902
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BJ705222 MF01FFA CDNA Oryzias latipes CDNA clone MF01FFA013a11 5', mRNA sequence.
BJ705222.1 GI:45246102
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                                                                                                                                                                                                                                                                                                                                                                                        Oryzias latipes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 413)
Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 729)

Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.

Medaka EST Project in Takeda's lab

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.0%; Score 17; DB 4; Length 729;
82.4%; Pred. No. 7e+02;
.ive 3; Mismatches 0; Indels
                            Score 17; DB 5; Leus-Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db xref="taxon:8090"
/clone="MF01FFA013a11"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="fry stage 40"
/clone_lib="MF01FFA CDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryzias latipes"
/mol_type="mRNA"
/strain="Hd-rR"
                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                      DST.
Oryzias latipes (Japanese medaka)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                         mRNA sequence.
BP569691
BP569691.1 GI:48985457
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                                    85.0%;
                                                                                                                    3 AGGGTCGAUGUCCAUGC
                                                                             14; Conservative
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                                      Query Match
Best Local Similarity
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KEYWORDS
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BJ705222/c
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TITLE
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Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
Sakajima,M., Enju,A., Akyyama,K., Oono,Y., Murametut,M.,
Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shihaqawa,A. and Shinozaki,K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
                                                                                                    1 (bases 1 to 260)
Gargy, D., Pearlman, R.B. and Carlton, J.
PEPGbyl, (http://amcobidia.bcm.umontreal.ca/public/pepdb/agrm.php)
Tetrahymena thermophila (TIGR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                       Tetrahymena thermophila
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
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reversed clone, Please visit our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 260;
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                                                                                                                                                                                                                Contact: PEPdb
Departement de Biochimie, Universite de Montreal
Email: pepdb-curator@bch.umontreal.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                       1. .260
/organism="Tetrahymena thermophila"
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                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Normalized large"
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Arabidopsis thaliana
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/tissue_type="mixture of
/lab_host="DH10B"
/clone_lib="RAFL19"
                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:5911"
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    CN589115.1 GI:47040917
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BP643309.1 GI:49294779
                                           Tetrahymena thermophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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Best Local Similarity
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Best Local Similarity 85.0 Matches 17; Conservative
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Best Local Similarity 75.0
Matches 15; Conservative
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Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M., Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y., Hayaswa, T., Shibata, K., Shinagawa, A. and Shinozaki, K. Functional annotation of a full-length Arabidopsis cDNA collection Science 296 (5565), 141-145 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 431)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PGIR (2003c)
Unpublished (2003)
Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.
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ZMMBBb0619B24r ZMMBBb (HindIII) Zea mays genomic clone
ZMMBB0619B24 3', genomic survey sequence.
                                                                                                                                             Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3.-1.1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
reversed clone; Please visit our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%; Score 16.8; DB 5; Length 413;
.larity 75.0%; Pred. No. 8.2e+02;
Conservative 3; Mismatches 2; Indels
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Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="root"
/lab_bost="DH108"
/clone_lib="Raph14"
/note="Site_l: BamH1; Site_2: Sall"

    .413
    /organism="Arabidopsis thaliana"

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Location/Qualifiers
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/cultivar="B73"
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                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 TAAGGGTTGATGTCCATGAC 402
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                                                                                                                                 Contact: Motoaki Seki
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CL260820
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Sukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Sukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Sukaryota, Viridiplantes, Solanaces; Solanacese; Nicotiana.

1 (bases 1 to 457)

2 1 (bases 1 to 457)

3 Matsucka,K., Tashiro,G., Horiguchi,T., Demura,T. and Fukuda,H.

Profiling growth-phase dependent gene expression of tobacco BY-2
cells by comprehensive microarray analysis

L Unpublished (2003)

Contact: Ken Matsucka
Morphogenesis Research Group

RIKEN Plant Science Center

1-7-2 Suchirocho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9573

Email: bylagepsc.riken.go.jp, URL:http://mrg.psc.riken.go.jp/strc/

The CDNA library was constructed from mRNA isolated from lag (9 h), log (72 h) and steationary (7 days) old BY-2 cells.
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Genomic survey sequence.
AL481016
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/lab host="E. coli DH10B"
/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="MAT001"
/note="Vector: pGEM-T easy; primer: M13 forward; mRNA
obtained from lag, log and stationary phase cells"
                                                                                                                                                                           Gaps
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                                                                                                                            Length 431;
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                                                                                                                  Score 16.8; DB 9;
Pred. No. 8.3e+02;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="Bright Yellow No.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Nicotiana tabacum"
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clone="BY12728"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 TAAAGTTCGATGTCCATGCC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell line="BY-2"
                                                                                                                                                                                                                      1 TAAGGGTCGAUGUCCAUGCC 20
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ORGANISM

REFERENCE AUTHORS TITLE

COMMENT

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/mol_type="mRNA"
/db xref="texon:9606"
/clone="luMAGE:2295092"
/tissue_type="adenocarcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 17-DEC-2002
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msh2 3006 y2 msh Pseudomonas aeruginosa genomic clone msh2_3006,
genomic survey sequence.
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1 (basea; Dr. 773)
Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M., Burns, J. L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
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/note="Environmental isolate. Whole genomic shotgun
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80.0%; Pred. No. 9e+02;
ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                     Query Match 84.0%; Score 16.8; DB 1; Length 733; Best Local Similarity 75.0%; Pred. No. 8.9e+02; Matches 15; Conservative 3; Mismatches 2; Indels
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Fax: 2066857244
Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="MSH"
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Location/Qualifiers
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/clone lib="msh"
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Pseudomonas aeruginosa
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AG476230/c
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BZ573222/c
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                                                                                                L (Jobers I to 307).

State I (Jobers I to 307).

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S. E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CBlo ISA, B-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
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Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lln.gov/bbrp/image/image.html
Insert Length: 1107 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
     Trypanosoma brucei
Bukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
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Pred. No. 8.5e+02;
2; Mismatches 2;
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/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="230401"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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High quality sequence stop: 401.
Location/Qualifiers
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Best Local Similarity 80.0%;
Matches 16; Conservative 7
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                                                         Trypanosoma.
1 (bases 1 to 509)
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Unpublished (1997)
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A1635930 LOCUS DEFINITION

RESULT 11

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Pan troglodytes
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                                                                                                                                                                                                                                                                            Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi, Fur, Yokohama, Kanagawa 230-0045, Japan Fel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-238-36-9189, fax: 81-238-36-9199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Solanum tuberosum (pocaco)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 272)
And der Hoveen, R. S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R.,
Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Unpublished (2000)
Contact: Robin Buell
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                         2 (bases 1 to 1574)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
                                                                                                                                                             Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-369C21.TJ"
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                   AG476230.1 GI:48183460
                                                         Mus musculus molossinus
Mus musculus molossinus
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BE922196.1 GI:10448260
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Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bloscience and Blotechnology (KRIBB), Genome Research Center (GRC);
Bloscience and Blotechnology (KRIBB), Genome Research Center (GRC);
E., Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail:kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Bmail: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/.
Location/Qualifiers
1. .27
//crganiem="Solanum tuberosum"
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Pan troglodytes DNA, clone: RP43-082P16.T7, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="potato leaves and petioles"
/note="Vector: pBlueScript SK(-); Site 1: EcoRl; Site 2:
Xhol; Tissue was supplied by Dr. Fry (Gornell University)
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="leaflets and petioles"
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R.Site 1 : ECORI
R.Site 2 : ECORI.
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AG200800.1 GI:45232975
GSS.
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Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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Search completed: March 17, 2005, 11:07:49 Job time : 1389.27 secs

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Run on:

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AY274428 Hepatitis
AY274430 Hepatitis
AY274431 Hepatitis
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AY274436 Hepatitis
AY382501 Hepatitis
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AY382504 Hepatitis
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AY38255 Hepatitis
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Unclassified.
11 (bases 1 to 30)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.
1 (bases 1 to 20)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
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Oligonucleotides specific for hepatitis B virus
Patent: US 5856459-A 15 05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Pred. No. 14;
3; Mismatches 0;
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Sequence 40 from patent US 5856459.
AR027842. GI:5938662
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Sequence 15 from patent US 5856459.
AR027817
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                                                                                                                                                                    AY382521
AY382522
AY382524
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AY382502
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85.0%; P
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Best Local Similarity 85.0
Matches 17; Conservative
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Unknown.
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AUTHORS
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AR027817
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AR027842
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S77749 preC {X/pre
A729529 Hepatitis
A732956 Hepatitis
A7329571 Hepatitis
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A8167601 Hepatitis
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A7254501 Hepatitis
A7274419 Hepatitis
A7274419 Hepatitis
                                                                                  March 17, 2005, 04:07:57; Search time 683.733 Seconds (without alignments) 1417.372 Million cell updates/sec
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AR027842 Sequence
AR027843 Sequence
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                                                                                                                                                                                                                                               9416466
            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                     4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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AY329562
AY329562
AY329563
AY3295010
HPBHBED
AB16763
AB16763
AB163815
AB163815
AB163815
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AY254503
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AR027842
AR027843
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Perfect score:
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Minimum DB Maximum DB

Database

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Gaps

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source

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FEATURES

DEFINITION

AR027843 LOCUS

RESULT 3

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

PEATURES

ORIGIN

ACCESSION VERSION KEYWORDS SOURCE

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Hepatitis B virus isolate A611252E X protein gene, partial cds; and A2129529 A129529
                                                                                                                                                                                                                                 Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 174)
Feitelson,M.A., Duan,L.X., Guo,J. and Blumberg,B.S.
X region deletion mutants associated with surface antigen-positive hepatitis B virus infections
Gastroenterology 108 (6), 1810-1819 (1995)
                                                                                                                 S77749
preC {X/preC region, deletion mutant} [hepatitis B virus HBV, host-human, serum, patient 5 isolate, Genomic DNA Mutant, 174 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUN-2003) Research & Development, Laboratorio Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo 01402-001, Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
Situns, R., Rebello Pinho, J.R., Bertolini, D.A., Bernardini, A.P.,
Situns, R., Rebello Pinho, F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in
Brazilian Patients
J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
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Rebello Pinho, J.R., Sitnik, R., Carrilho, F.J., Da Silva, L.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                               GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 165980] from the original journal article. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69. .. > 174
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/note="no start codon found"
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     71 TAAGGGTCGATGTCCATGCC 52
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100.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative 3;
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                                                                                                                                                                         ACCESSION
VERSION
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AY329529/c
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Unclassified.
I (bases 1 to 30)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
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                                                                                                                                                                             6; Length 30;
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Mills,J.S.
Oligonucleorides specific for hepatitis B virus
Patent: US 5856459-A 40 05-JAN-1999;
Location/Qualifiers
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Oligonucleotides specific for hepatitis B virus
Patent: US 5856459-A 41 05-JAN-1999;
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Best Local Similarity 85.0%; Pred. No. 14;
Matches 17; Conservative 3; Mismatches
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1 (bases 1 to 81)

Carmichael, B.
Antiviral poly-and oligonucleotides
Patent: US 5728518-A 9 17-MAR-1998;
Location/Qualifiers
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Sequence 41 from patent US 5856459.
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ACCESSION VERSION KEYWORDS

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Hepatitis B virus isolate D604917E X protein gene, partial cds; and preC/C protein gene, complete cds. AY329573
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                                                                                                                                                      AY329568 253 bp DNA linear VRL 08-JUN-2004 Hepatitis B virus isolate D296668E X protein gene, partial cds; and
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Sitnik, R., Rebello Pinho, J.R., Bertolini, D.A., Bernardini, A.P., Silva, L.C. and Carrilho, F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 253)
Rebello Pinho,J.R., Sitnik,R., Carrilho,F.J., Da Silva,L.C. and
Bernardini,A.P.
Gaps
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hepatitis B virus"
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 3; Mismatches
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Best Local Similarity 85.0%; R
Matches 17; Conservative 3;
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 253)
Sitnik, R., Rebello Pinho, J. R., Bertolini, D. A., Bernardini, A. P., Silva, L. C. and Carrilho, F. J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in
Brazilian Patients
J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
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Submitted (23-JUN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao E
01402-001, Brazil
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                                                                                                                                                                                                                                                                             Length 253;
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1. 253
/organism="Hepatitis B virus"
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Pred. No. 17;
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17; Conservative 3;
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Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., Da
Silva,L.C. and Carrilho,F.J.
                                                                                                                                                               Direct Submission
Submitted (13-UN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
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Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
Location/Qualifiers
            Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., Slva,L.C. and Carrilho,F.J. Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
                                                                                                                            Rebello Pinho,J.R., Sitnik,R., Carrilho,F.J., Da Silva,L.C. and Bernardini,A.P.
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/codon_start=3
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AF390000 294 bp DNA linear VRL 06-MAR-2002 Hepatitis B virus isolate D3 X protein gene, partial cds; and nonfunctional precore/core protein gene, partial sequence.
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95. .. >29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses; Hepadnaviridae, Orthohepadnavirus.
Viruses, Lo 294)
Castro, L.D., Niel, C. and Gomes, S.A.
Low frequency of mutations in the core promoter and precore regions of Microtis B virus in anti-HBe positive Brazilian carriers
BMC Microbiol. 1 (1), 10 (2001)
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De Castro,L., Niel,C. and Gomes,S.A.

Direct Submission

Submitted (Il-JUN-2001) Virology, FIOCRUZ, Av. Brasil 4365, Rio de Janeiro, RJ 21045-900, Brazil

Location/Qualifiers
                                                                                                                                                                                                      Gaps
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                                                                                                                                                             253;
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/db_xref="GI:37628472"
/trānslation="MQLFHLCLIISCSCPTVQASKLCLGWL"
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/mol_type="qenomic DNA"
/isolate="D3"
                                                                                                                                                             DB
                                                                                                                                                        Query Match
100.0%; Score 20; DE
Best Local Similarity 85.0%; Pred. No. 17;
Matches 17; Conservative 3; Mismatches
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Pred. No. 17;
3; Mismatches
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Hepatitis B virus gene for polyprotein, partial cds, clone: NEP27. AB167637
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LSFLPSDFFPSVRDLLDTASALYREAL"
                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MQLFHLCLIISCTCPTFQASKLCLGWLWGMDIDPYKBFGATVBL
LSFLPSDFFPSVRDLLDTASALYRBAL"
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Submitted (15-WAR-2004) Yasuhito Tanaka, Nagoya City University
Graduate School of Medical Sciences, Department of Clinical
Molecular Informative Medicine; 1 Kawasumi, Mizuho-cho, Mizuho-ku,
Nagoya, Aichi 467-8601, Japan (E-mail:ytanaka@med.nagoya-cu.ac.jp,
Tel:81-52-853-8292, Fax:81-52-842-0021)
Location/Qualiflers
2 (bases 1 to 398)
Tanaka,Y. and Mizokami,M.
Direct Submission
Submitted (15-MAR-2004) Yasuhito Tanaka, Nagoya City University
Graduate School of Medical Sciences, Department of Clinical
Molecular Informative Medicine, I Kawasumi, Mizuho-cho, Mizuho-ku,
Nagoya, Aichi 467-8601, Japan (B-mail:ytanaka@med.nagoya-cu.ac.jp,
Tel:81.52-853-8292, Fax:81-52-842-0021)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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                                                                                                                                                                                               /organism="Hepatitis B virus"
/mol_type="genomic DNA"
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184. .>39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hepatitis B virus"
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/db_xref="taxon:10407"
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/db_xref="G1:53148361"
                                                                                                                                                                                                                                                                                                                                             /product="polyprotein"
/protein_id="BAD52175.1"
/db_xref="G1:53148167"
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Tanaka, Y. and Mizokami, M.
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184. .>398
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85.0%; E
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AB167637/c
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                                                                                                                                                                                                                                 Tong.S.P., Li,J.S., Vitvitski,L. and Trepo,C. Active hepatitis B virus replication in the presence of anti-HBe is associated with viral variants containing an inactive pre-C region Virology 176 (2), 596-603 (1990)
                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 333)
Li,J.S., Tong,S.P., Wen,Y.M., Vitvitski,L., Zhang,Q. and Trepo,C.
Hepatitis B virus genotype A rarely circulates as an HBe-minus
mutant: possible contribution of a single nucleotide in the precore
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                                         HPBHBED 333 bp DNA linear VRL 28-JUN-1996 Hepatitis B virus precore and core protein gene, 5' end of cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MDIDPYKERGATVELLTFLPSDFFPSVRDLLDTAAALYREALES
PEHCSHHHTALRQAILCWGELMTLATWVGANLDDPASR"
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                                                                                                                    HBCAg protein; HBeAg protein; core protein; nucleotide binding protein; precore protein. Hepatitis 8 virus Hepatitis B virus
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Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
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/mol_type="genomic DNA"
/db_xref="taxon:10407"
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAB03102.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .>333
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/standard_name="HBcAb"
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AB167603.1 GI:53148166
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Matches 17; Conservative
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  RESULT 12
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Labers 1 to 406)
Hasegawa,I., Tanaka,Y. and Mizokami,M.
Direct Submission

Submitted (24-FEB-2004) Izumi Hasegawa, Nagoya City University
Graduate School, Department of Internal Medicine and Molecular
Science: 1 Kawasumi, Mizuho-cho, Mizuho-ku, Nagoya, Aichi 467-8601,
Japan (E-mail:izu-hase@med.nagoya-cu.ac.jp, Tel:81-52-853-8216,
Fax:81-52-852-0849)
I. . 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="OldpkyLHKRTLGLPAMSTTDLEAYFKDCVFKDWBELGEETRLM
IFVLGGCRHKLVCAPSSCNFFTSA"
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/translation="WQLFHGLISCTCPTVQASKLCLGWLWGMDIDPYKEFGATVEL
LSFLPQDFFPSVRDLLDTASALYREALESP"
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                                                                                                                                                                                               AB163815 406 bp DNA linear VRL 29-JUN-2004 Hepatitis B virus X, preC/C genes for polyproteins, isolate:
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Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
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J. Virol. 78 (14), 7575-7581 (2004)
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/mol type="genomic DNA"
/isoTate="SAF662"
                      3; Mismatches
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/db_xref="G1:49387445"
Best Local Similarity 85.0%; Pred. No. Matches 17; Conservative 3; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10407"
1. .208
                                                                              287 TAAGGGTCGATGTCCATGCC 268
                                                          TAAGGGUCGAUGUCCATGCC 20
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<1. .208
/gene="X"
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184. .>406
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/codon_start=1
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AB163815.1 GI:49387444
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Job time : 683.733 secs

Search completed: March 17, 2005, 08:14:17

287 TAAGGGTCGATGTCCATGCC 268

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Aan33072 Sequence
Aad31765 Hepatitis
Aca62422 Hepatitis
Aad60866 Hepatitis
Aas16094 HBV viral
Aas16092 HBV viral
Aas16093 HBV viral
Ad194544 SDMCOre d
Ad789273 Lab-on-ch
Ad789266 Lab-on-ch
Aad789266 Lab-on-ch
Aad78926 Lab-on-ch
Aad45813 HBV JMA2
Aaq46961 PCR prime
Adq46961 PCR prime
Abk673206 Hepatitis
Ada83206 PCR prime
Abk67329 Primer #1
Abk67329 Primer #1
Abk67329 Primer #2
Ad8680023 Primer fo
Ad8610976 Chimeric
Adq46965 PCR prime

Title: Perfect score:

Sequence:

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Run

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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The present sequence represents a synthetic oligonucleotide HBV92b which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a
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/note= "Internucleotide linkages are phosphorothioate"
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ADJ94545
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ADJ9273
ADR89266
AAQ45813
AAQ6723
AAQ66723
ADG46961
ADM83206
ADK67432
ADK67432
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ADE80023
ADE10976
ADG46965
ADM83210
                 ACA62422
AAD60866
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AAS16092
AAS16093
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Roberts NA, Roberts PC, Slade A;
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Aad27422 Hepatitis
Aad37509 Hepatitis
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Aad07220 Hepatitis
Aav82691 Fulminant
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Aat72573 Hepatitis
Aat72619 Hepatitis
Aat72620 Hepatitis
Aat72618 Hepatitis
Aat72621 Hepatitis
                                                          March 17, 2005, 04:03:33 ; Search time 171.333 Seconds (without alignments) 691.020 Million cell updates/sec
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sample. The antisense oligonucleotide, and oligonucleotides containing a agequence which is complementary to at least two non- contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
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"Internucleotide linkages are phosphorothioate"
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100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.5;
Matches 17; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                  Hepatitis B virus RNA antisense oligonucleotide HBV92Mb.
                                     Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
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/note= "2'-0-methyladenosine"
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/note= "2'-OMe RNA"
                                                                                 AAT72573 standard; DNA; 20 BP
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mod_base= um
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The present sequence represents a synthetic oligonucleotide HBV92Mb which is complementary to a portion of the hepatitis B virus' (HBV) RMA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non- contiguous regions of an HBV uncleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
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"Internucleotide linkages are phosphorothioate"
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mod_base= OTHER
note= "2'-0-methyladenosine"
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/note= "2'-OMe RNA"
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/mod_base= OTHER
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/mod_base= gm
96WO-EP002432
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Roberts NA, Roberts PC,
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Best Local Similarity 90.0"
Fra 18; Conservative
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          The present sequence represents a synthetic oligonucleotide HBV-90Mb which contains a sequence which is complementary to at least two noncontiquous regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
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/note= "Internucleotide linkages are phosphorothioate"
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Matches 17; Conservative
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Roberts NA,
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/mod_base= OTHER
/note= "2'-O-methyladenosine"
                                                                                                                                                                 note= "2'-0-methyladenosine"
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'note= "2'-OMe RNA"
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                                                                                                                                                    base= OTHER
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'mod_base= gm
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Roberts NA, Roberts PC,
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Gaps

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Claim 5; Page 15; 81pp; English

RESULT

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The present sequence represents a synthetic oligonucleotide HBV-91Mb which contains a sequence which is complementary to at least two noncontiguous regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                *tag= a
'note= "Internucleotide linkages are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R, Kilkuskie RE, Mills JS;
Hepatitis B virus RNA antisense oligonucleotide HBV-91Mb
                            HBV; HBV infection; inhibition; replication; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "2'-0-methyladenosine
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                                                                                     Location/Qualifiers
                                                                                                                                         21. .30
/*tag= b
/note= "2'-OMe RNA"
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PC, Slade A;
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/mod_base= cm
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Roberts NA,
                                                                                                    misc_feature
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                                                         Synthetic
                                                                                                                                             misc RNA
                                                                                       Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a synthetic oligonucleotide HBV-90b which contains a sequence which is complementary to at least two non-contiguous regions of a hepatitis B virus (HBV) mucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication in a sell or for the treatment of HBV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                                                                                                                                                                                                                      /*tag= a
/note= "Internucleotide linkages are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mills JS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kilkuskie RE,
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85.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                   Hepatitis B virus RNA antisense oligonucleotide HBV-90b.
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                                                                                                                                                                                                                              HBV; HBV infection; inhibition; replication; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jupp R,
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                                                                                                                                                                                                                                                                                        cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goodchild J,
PC, Slade A;
                            TAAGGGUCGAUGUCCATGCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 TAAGGGTCGATGTCCATGCC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TAAGGGUCGAUGUCCATGCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 15; 81pp; English
                                                                                                               AAT72618 standard; DNA; 30 BP
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                                                                                                                                                                       (first entry)
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Roberts NA, Roberts PC,
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04-SEP-1997 (first entry)

AAT72621;

RESULT 6
AAT72621
ID AAT7.
XX
AC AAT7.
XX
DT 04-S.

Query Match Matches

ò 셤 Location/Qualifiers

/product= "HBcAg"

/*tag= a

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prophylactic; gene therapy, vaccine; hepatitis A wirus; HAV; herpes; hepatitis C virus; HAV; nafluenza; foot-and-mouth disease; diarrhoea; tuberculosis; polio; rabies; acquired immunodeficiency syndrome; AIDS; dengue fever; yellow fever; malaria; whooping cough; salmonellosis; antiprotozoal; ds.
                      B virus; HBV; core antigen; HBcAg; immune system; typhoid;
Hepatitis B virus (HBV) core antigen (HBcAg) encoding DNA #1.
                                                                                                                                                                                                                                                                  22-JUN-2000; 2000GB-00015308.
06-OCT-2000; 2000GB-00024544.
                                                                                                                                                                                                                                            22-JUN-2001; 2001WO-GB002817.
                                                                                                                                                                                                                                                                                                     (CELL-) CELLTECH PHARM LTD.
                                                                                                                                                                                                                                                                                                                           Page M, Li J, Pumpens P;
                                                                                                                                                                                                                                                                                                                                                 2002-098223/13.
                                                                                                               Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAE17018.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening of antiviral agents by protein-priming activity of hepatitis B virus DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method of screening for an antiviral agent by the protein-priming activity of hepatitis B virus (HBV) DNA polymerase. Also described is developing an antiviral agent with a high selectivity to HBV which can be used for high-throughput screening. The present sequence represents an RNA oligonucleotide which is used in the
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                       screening; antiviral; hepatitis B virus; HBV; DNA polymerase; ss.
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                                                                                                                                                                                                                                Hepatitis B virus DNA polymerase related RNA oligonucleotide.
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                               ; Score 20; DB 2; Length 30;
Pred. No. 2.6;
2; Mismatches 0; Indels
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            Sequence 30 BP; 7 A; 6 C; 11 G; 3 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31 BP; 10 A; 6 C; 8 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ryu WS,
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Min MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 12; 13pp; Korean.
                                                                                          11 TAAGGGTCGAUGUCCAUGCC 30
                                                                                                                                                                                                                                                                                                                                                                                                         (MOGA-) MOGAM BIOTECHNOLOGY INST. (VIRO-) VIROGEN CO LTD.
                                                                              1 TAAGGGUCGAUGUCCATGCC 20
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                                                                                                                                                             ADC64743 standard; RNA; 31 BP
                                 100.08;
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                                            Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ji HJ, Jung SI, Kim YC,
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                                                                                                                                                                                                         18-DEC-2003
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                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                    ADC64743;
                                  Query Match
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The invention relates to modified proteins comprising hepatitis B virus (HBV) core antigen (HBCAg) wherein one or more of the four arginine repeats has been deleted and the protein comprising the C-terminal cysteine of HBCAg. The deleted region may be replaced by an epitope from a protein other than HBCAg, in which case the HBCAg acts as a carrier to present the epitope to the immune system. This chimeric protein or its nucleic acid is useful as a vaccine or in a method of prophylactic or therapeutic vaccination of the human or animal body, particularly against therapeutic vaccination of the human or animal body, particularly against they we constituted a vaccination of the chimeric protein any be used in gene therapy or DNA vaccination protocols. The chimeric protein or its nucleic acid may also be used as the basis of a prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth disease, polio, herpes, rables, acquired immunodeficiency syndrome (AIDS), dengue fever, yellow fever, malaria, tuberculosis, whooping cough, salmonellosis, typhoid, food poisoning,
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        antigen, useful as a
of the human or animal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diarrhoea, meningitis or gonorrhea. The present sequence is a DNA encoding Hepatitis B virus core antigen (HBCAg)
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Pred. No. 3.3;
3; Mismatches 0; Indels
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New proteins comprising a modified hepatitis B core ant vaccine in prophylactic or therapeutic vaccination of t body, particularly against hepatitis B virus infection.
                                                                                                                                                             Disclosure; Page 38-39; 40pp; English.
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AAD31509 standard; DNA; 639 BP.
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85.0%; E
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Best Local Similarity 85.0
Matches 17; Conservative
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BP.

AAD27422 standard; DNA; 639

18-APR-2002 (first entry)

AAD27422;

RESULT 8
AAD27422/C
1D AAD274;
XX
AC AAD274;
XX
DT 18-APR
XX

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This invention describes a novel particle (A), comprising a protein coat with a fusion protein (FP), and, inside the coat, a nucleic acid (I) including the sequence for a virus-specific packaging signal (FB) and a structural gene. FP contains a virus protein (VP), a peptide (P) that mediates cell permeability and a heterologous cell-specific binding site (RGD). The invention also describes (I) producing (A) in which FP contains an LHBs (large surface protein of hepatitis B virus (HBV)) and RGD; (2) preparing (A) in which FP contains an HBV core antigen (HBCAG), (P) and RGD; (3) FP; (4) DNA encoding FP; and (5) expression vector containing the DNA of (d). The products of the invention are used in gene therapy of cells and tissues, in vivo or ex vivo. This sequence encodes a fusion protein which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Particle for cell-specific gene delivery, useful in gene therapy, comprises nucleic acid in protein coat that includes a fusion protein of viral protein, permeability peptide and cell-binding site.
                                    Pusion protein; protein coat; virus-specific packaging signal; psi
virus protein; cell permeability; cell-specific binding site; LHB;
large surface protein; core antigen; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 663 BP; 154 A; 169 C; 152 G; 188 T; 0 U; 0 Other;
HBV fusion protein comprising LHB and RGD encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB
85.0%; Pred. No. 3.3;
ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HBcAg; immunomodulator; vaccine; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus core antigen DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10. .669
/*tag= a
/product= "HBCAg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
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ID ADO07220 standard; DNA; 669 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16a; Fig 1; 34pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 TAAGGGTCGATGTCCATGCC
                                                                                                                                                                                                                                                                  04-FEB-2000; 2000WO-DE000363
                                                                                                                                                                                                                                                                                                         99DE-01004800
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                                                                                                                                                                                                                                                                                                                                                                                          Hofschneider P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-514959/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus.
                                                                                                                       Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAB10596
                                                                                                                                                                                   WO200046376-A2
                                                                                                                                                                                                                                                                                                                                                  (HILD/) HILDT
                                                                                                                                                                                                                                                                                                         05-FEB-1999;
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                                                                                                                                                                                                                            10-AUG-2000
                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                          Hildt E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AD007220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to hepatitis B virus (HBV) core antigen (HBCAg) fusion proteins and polynucleotides encoding such proteins. Sequences of the invention are useful in methods of prophylactic or therapeutic vaccination or to manufacture medicaments for prophylactic or therapeutic vaccination of the human or animal body against HBV, e.g. against viral hepatitis. They are also useful as a prophylactic vaccine against e.g. hepatitis c virus, influenca, polio, herpes, rabies, acquired immune deficiency syndrome (AIDS) or foot-and-mouth disease. The present sequence is a DNA encoding hepatitis B virus core antigen (HBCAg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B (HB) core antigen fusion proteins, useful as vaccines for the prophylactic or therapeutic treatment of humans or animals against e.g. HB virus, viral hepatitis, hepatitis C virus, influenza, or foot-and-
                                                                                                Hepatitis B virus core antigen; HBcAg; prophylactic; viral hepatitis; therapeutic; vaccine; acquired immune deficiency syndrome; influenza; polio; herpes; rabies; AIDS; foot-and-mouth disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                         Hepatitis B virus core antigen (HBcAg) encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/product= "Mature HBc protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rowlands D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                /*tag= a
/product= "HBc protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 23-24; 27pp; English.
                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stuart D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-2001; 2001WO-GB001607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-APR-2000; 2000EP-00107118
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Best Local Similarity 85.0%;
Matches 17; Conservative
                   (first entry)
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                                                                                                                                                                                                                                                                                                                                             88. .636
/*tag= c
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                                                                                                                                                                                                                                             1. .639
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MEDE-) MEDEVA EURO LID
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                                                                                                                                                                                                                                                                                                             .87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gilbert R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-239995/29.
P-PSDB; AAE19793.
                                                                                                                                                                                 Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200177158-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouth disease.
                   18-JUN-2002
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08-JAN-2001
                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                  mat_peptide
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Gehin A,

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Gaps

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Indels

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AAA71734;

RESULT 10
AAA71734/c
ID AAA71
XX
AC AAA71
DT 06-AU
DT 08-JA

셤 ò

DB 3; Length 663;

15-0CT-1998

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The response to a peptide in a mammal comprises transmucosally administering to the mammal a macromolecular aggregate of the peptide. The macromolecular aggregate of the peptide The macromolecular aggregate comprises at least 10 peptide subunits, may have macromolecular aggregate comprises at least 10 peptide subunits, may have a molecular weight of over 1,000 kDa, and is preferably at least 5 nm in diameter. It is resistant to digestive degradation, being stabilised in aggregate form by chemical treatment and/or by recombinant protein aggregate form HBV surface protein, nucleocapsid protein or envelope protein. Transmucosal administration to a mammal of a mammal involves transmucosally administration and minimum response in the mammal. A method of suppressing a monomolecular peptide in a mammal involves transmucosally administering a monomolecular peptide that is resistant to digestive degradation and which may be stabilised by chemical treatment or protein engineering, and which may be stabilised by chemical treatment or protein engineering, and which may be derived from a HBV protein. A monomolecular peptide is useful for the induction of oral tolerance when induction of systemic immunity is undesirable, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the DNA sequence of the hepatitis B virus core antigen (HBcAg) gene from HBV serotype ayw. A peptide comprising a HBV protein can be used in claimed methods of the invention for modulating an immune response in a mammal. A method of inducing a systemic immune
                                                                                                                                                                                                                                                                                                                                                   Modulating a systemic immune response to a peptide in a mammal comprises transmucosally administering a macromolecular aggregate of the peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 12; Length 669; 85.0%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 669 BP; 155 A; 170 C; 148 G; 196 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                  /note= "No start codon"
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 TAAGGGTCGATGTCCATGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TAAGGUCGAUGUCCATGCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :691/c
AAV82691 standard; DNA; 1334 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in cases of chronic infections.
                                                                                                                                   17-OCT-2003; 2003WO-US033178
                                                                                                                                                                          17-OCT-2002; 2002US-0419279P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-PEB-1999 (first entry)
/partial
                                                                                                                                                                                                                                                                                            WPI: 2004-348329/32.
                                                                                                                                                                                                             (ORAG-) ORAGEN CORP
                                                                                                                                                                                                                                                                                                              P-PSDB; AD007221
                                                          WO2004035007-A2
                                                                                             29-APR-2004
                                                                                                                                                                                                                                                     Michaels F;
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Pulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;

HBV-related disease; ss.

Hepatitis B virus

WO9845421-A2

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The present sequence represents part of the genome of a fulminant
Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
The specification describes Hepatitis B virus (HBV) nucleic acid that has
a mutation (i.e. alteration from the normal nucleotide in any of the
c quotypes A to F) in at least two of the enhancer I region, the negative
c genotypes A to F) in at least two of the enhancer I region, the negative
c genotypes A to F) in at least two of the enhancer II core upstream region, the negative
c genotypes A to F) in at least two of the enhancer II core upstream region.

C genotypes A to F) in at least two of the enhancer II core upstream region.

C genotypes A to F) in at least two of the enhancer II core upstream region which leads to an X-
peptide amino acid change to Cys or Met. The HBV variants of the
c peptide amino acid change to Cys or Met. The HBV variants of the
c proteins and HBV nucleic acid. Probes that hybridise to any of the
c specified mutated regions are used to detect HBV-related disease,
c specified mutated regions are used to detect HBV-related disease.

C specified mutated forms of disease. Combinations of the specified
c mutations are associated with fulminant infections, probably because they
creduce the ability to bind inhibitory proteins in the host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatitis B virus; variant; FHBV; HBV; binding interaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1334 BP; 288 A; 363 C; 311 G; 372 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20; DB 2
No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    806 TAAGGGTCGATGTCCATGCC 787
                                                                                                                                                                                                                                                                                         Disclosure; Fig 5; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TAAGGGUCGAUGUCCATGCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV82688 standard; DNA; 1395 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
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                                   98WO-EP002048
                                                                      97GB-00007221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HBV-related disease; ss.
                                                                                                                                                                                WPI; 1999-009329/01.
                                                                                                        (UNIU ) UNIV GLASGOW
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                                   08-APR-1998;
                                                                       09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9845421-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV82688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV82688/c
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8X#X#X#X#X#X#####
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Hepatitis B vius (FHN) genous products and considerable because the specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleic acid that has genotypes A to P) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic. present sequence represents part of the genome of a fulminant Sequence 1395 BP; 277 A; 387 C; 331 G; 398 T; 0 U; 2 Other; Disclosure; Fig 5; 85pp; English

100.0%; Score 20; DB 2; Length 1395; 85.0%; Pred. No. 3.5; Pred. No. 3.5; 3; Mismatches 917 TAAGGGTCGATGTCCATGCC 898 1 TAAGGGUCGAUGUCCATGCC 20 Local Similarity 85.0 es 17; Conservative Query Match Matches

AAV82687 standard; DNA; 1400 BP 16-FEB-1999 (first entry) AAV82687; RESULT 14
AAV82687/c
AAC AAV82
XX AAV82
DT 16-FE
XX FULMI
XX FULMI
XX HBV-1
XX HCPA
XX

Fulminant hepatitis B virus, variant, FHBV, HBV, binding interaction, HBV-related disease, ss. Fulminant hepatitis B virus genotype D variant FHBV4 sequence.

Hepatitis B virus.

WO9845421-A2

15-OCT-1998

98WO-EP002048 08-APR-1998; 97GB-00007221 09-APR-1997;

(UNIU) UNIV GLASGOW

Carman B;

WPI; 1999-009329/01.

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure, Fig 5, 85pp, English.

The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the

because they regulatory element region, the enhancer II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV related disease, especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell genotypes A to F) in at least two of the enhancer I region, the negative 886666666666888

Sequence 1400 BP; 287 A; 388 C; 332 G; 393 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 20; DB 2; Length 1400; 85.0%; Pred. No. 3.5; Indels ° Pred. No. 3.5; 3; Mismatches Best Local Similarity 85.0 Matches 17; Conservative Query Match

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AAV82692 standard; DNA; 1445 BP

(first entry) 16-FEB-1999 AAV82692;

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Gaps

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0; Indels

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction; Fulminant hepatitis B virus genotype D variant FHBV13 sequence HBV-related disease; ss.

Hepatitis B virus.

15-0CT-1998

98WO-EP002048 08-APR-1998; 97GB-00007221. 09-APR-1997;

(UNIU) UNIV GLASGOW

Carman B;

WPI; 1999-009329/01.

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure, Fig 5; 85pp; English

The present sequence represents part of the genome of a fulminant
Hepatitis B virus (FHBV) genotype D variant, nuclectides 1000 to 2500.
The specification describes Hepatitis B virus (HBV) nucleic acid that has
a mutation (i.e. alteration from the normal nucleotide in any of the
genotypes A to F) in at least two of the enhancer I region, the negative
cequence/ basal core promoter region, or a mutation which leads to an Xpeptide amino acid change to Cys or Met. The HBV variants of the
peptide amino acid change to Cys or Met. The HBV variants of the
ceptide amino acid detect binding interactions between host or viral
proteins and HBV nucleic acid. Probes that hybridise to any of the
specified mutated regions are used to detect HBV-related disease,
specified mutated regions are used combinations of the specified
serologically fulminant infection, but also severe chronic infection or
serologically nunsual forms of disease. Combinations of the specified
mutations are associated with fulminant infections, probably because they
reduce the ability to bind inhibitory proteins in the host cell

Sequence 1445 BP; 297 A; 406 C; 338 G; 404 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1445; Best Local Similarity 85.0%; Pred. No. 3.5; Matches 17; Conservative 3; Mismatches 0; Indels 0 ò

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0; Gaps

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Search completed: March 17, 2005, 06:48:43 Job time : 171.333 secs

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March 17, 2005, 05:44:58; Search time 1386.27 Seconds (without alignments) 549.162 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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| AG128210 Pan trogl BH257005 CH230-283 CO099982 GR Ea25C BJ571152 BJ571152 CG289400 CGXBN55TV CG875596 ZWMBBC028 CC622611 OGULP56TV CL055525 CH216-81E AL110272 Homo Bapi AL110272 Homo Bapi AL137702 Homo Bapi BIO52244 PN2-GN037 BIO52244 PN2-GN037 BIO52209 PN2-GN037 BX433931 BX433931 CG106546 PUIJU59TB BZ413874 if18410.9 CG255822 CGWKA72TV CG255820 OGUKA72TV CG255820 OGTA138TC CG2658 CGTA138TC CG265772 OGICX72TH | ENTS mRNA linear EST 19-OCT-2001 green seedling EST library Hordeum vulgare subsp. vulgare cDNA puence. i,A., Wise,R., Chin,A., Begum,D., liliopsida; Poales; Poaceae; i,A., Wise,R., Chin,A., Begum,D., lenry,D., Palmer,M., Rambo,T., nd physically anchored EST resource infected Morex (compatible) seedling stitute i66 66 66 1. igare subsp. vulgare" ligare subsp. vulgare" | seedling leaf" vulgare green seedling EST library infected)" script SK(-); Site_1: EcoRI; Site_2: ants were greenhouse grown in the R |
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| AG128210 BH257005 CO09982 BJ571152 CG289400 CG289400 CG8975596 CG285211 CC65525 HSM802167 BSM802167 BSM802167 BSM802167 BSM802167 BSM802167 CG106546 CG106546 CG2558210 CG258810 CG258810 CG258810 CG257272 CG302315 BH631190 | ALIGNM 686 by infected) infected) 646 o. vulgare intes; Sundare liophyta; Hordeum. Kleinhofs, and Main, Hordeum setically an Blumeria : edu seto, SC 29 alifiers fordeum vu mson, SC 29 alifiers | memoraci.r. e="green seedlin. TJC121" "Hordeum vulgare (Blumeria infect. or: pBluescript ; (mla) plants we |
| 714 9 848 7 9 851 9 10010 9 | B1954819 B1954819 B1954819 HVSDMA0014 (Blumeria infected) clone HVSMEm0019017f, mRNA sequence HVcDMA0014 (Blumeria infected) clone HVSMEm0019017f, mRNA sequence B1954819.1 GI:16300646 EST. Hordeum vulgare subsp. vulgare B1954819. Viridiplantae; Stree Spermatophyta; Magnoliophyta; Joharavota; Viridiplantae; Stree Spermatophyta; Magnoliophyta; Joharavota; Viridiplantae; Stree Spermatophyta; Magnoliophyta; Joharavota; Viridiplantae; Streen, D., Akkins, M., Yu, Y., H. Frisch, D., Akkins, M., Yu, Y., H. Simmons, J., Oates, R. and Main, Development of a genetically a for barley genomics: Blumeria: contact: Wing RA Clemson University Genomics Inclemson University Genomics Seq Primer: AATTAACCCTCACTAAAGG High quality sequence state: 1, 100 duality sequence stop: 53 Location/Qualifiers Inclemson Lype="MRNA" (cultivar="Mones" Joha Species="Vulgare Joha Stref="Erexon:11250" Joha = "HUSMEMONI 9017" Joha = "HUSMEMONI 901 | /clone="Normanousgraph"/ tissue_type="green /lab_host="TJC12" /clone_lib="Hordeum HYCDNA0014 (Blumeria /note="Vector: pBlue XhoI; Morex (mla) pl |
| 16.4 82. 16.4 82. 16.4 82. 16.4 82. 16.4 82. 16.4 82. 16.4 82. 16.4 82. 16.4 82. 16.8 80. 16 80. 16 80. 16 80. 16 80. 16 80. 16 80. 16 80. 17 80. 18 80. 18 80. 19 80. 10 80. 11 80. 11 80. 12 80. 13 80. 14 80. 16 80. 17 80. 18 80. 18 80. 19 80. 10 80. 11 80. 11 80. 12 80. 13 80. 14 80. 15 80. 16 80. 17 80. 18 | o o | |
| 0 0 . 00 000 22 22 22 22 22 22 23 24 24 24 24 24 24 24 24 24 24 24 24 24 | RESULT 1 B1954819/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE TITLE JOURNAL COMMENT REATURES SOURCE SOURCE AUTHORS | |

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Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria grammlis f. sp. hordel, and leaves were harvested 24, 48 and 72 hr post-inoculation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Aktins and Wing). Plasmid DNA preparations, DNA sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis sequence analysis sequence and interval.
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ZMMBBb00002P18.r ZMMBBb Zea mays genomic clone ZMMBBb0002P18 3',
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Yu.Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J. and Wing,R.
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Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically hybsically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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Tel: 520 626 3967
Fax: 520 621 9288
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CN589115 260 bp mRNA linear EST 31-AUG-2004 TTE00013587 Normalized large Tetrahymena thermophila cDNA, mRNA cN589115
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Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuke,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PGIR (2003c)
Unpublished (2003)
Contact: Bharti,A.K.
Dr.Joachim Messing's lab
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                                                                                                                                    87.0%; Score 17.4; DB 8;
84.2%; Pred. No. 4.2e+02;
iive 2; Mismatches 1;
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3; Mismatches 1;
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1. .763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
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Fax: 732 445 5735
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Gaps

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Length 451 0; Indels

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PP569691 BP569691 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-68-M24 3', BP569691 RAFL14-68-M24 3', BP569691
                                                                                                                                                                                                                                                HJ705222 MF01FFA CDNA Oryzias latipes CDNA clone MF01FFA013a11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Core corosids; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 413)
Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
estinopecarygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha,
Beloniformes, Adrianichthyidae, Oryziinae, Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 729)
Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 85.0%; Score 17; DB 4; Length 729; Best Local Similarity 82.4%; Pred. No. 7e+02; Matches 14; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      male"
                                  Score 17; DB 5; 1
Pred. No. 6.5e+02;
3; Mismatches 0;
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/eex="mixture of female and itissue_type="whole embryo"
/dev_stage="fry stage 40"
/clone_lib="MF01FFA cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Oryzias latipes"
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                                                                                                                                                                                                                                                                                                                                                                                            Oryzias latipes (Japanese medaka)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="taxon:8090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="Hd-rR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 AGGTCGATGTCCATGC 447
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                                    85.0%;
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BJ705222/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T., Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M., Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishij, Y., Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K. Functional annotation of a full-length Arabidopsis cDNA collection Science 296 (5565), 141-145 (2002)
                                                                                                       T. (Dases 1 to 260)

Garg,J., Pearlman,R.E. and Carlton,J.
PERGDPU, (http://amcebidia.bcm.umontreal.ca/public/pepdb/agrm.php)
Tetrahymena thermophila (TIGR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.
(bases 1 to 451)
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                                      Tetrahymena thermophila
Butertahymena thermophila
Bukaryota; Jahermophila
Bukaryota; Jahermophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
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reversed clone; please visit our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFLi9-61-108"
/tissue_type="mixture of silique and flower"
/lab_host="DH108"
/clone_lib="RAFLi9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                          Contact: PEPdb
Departement de Biochimie, Universite de Montreal
Email: pepdb-curator@bch.umontreal.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Motoaki Seki
Plant Punctional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Teukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                    1. .260
/organism="Tetrahymena thermophila"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.0%; Score 17; DB 7; 82.4%; Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Normalized large"
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Arabidopsis thaliana
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/db_xref="taxon:5911"
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BP643309.1 GI:49294779
CN589115.1 GI:47040917
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Trypanosoma brucei
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1 (bases 1 to 431)

Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C., Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.
Sequencing of the maize genome at PGIR (2003c)
Unpublished (2003)

Contact: Bharti, A.K.
Dr. Joachim Messing's lab

The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
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Nakajima,M., Enju,A., Akiyama,K., Oono,Y., Muramatsu,M., Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K. Functional annotation of a full-length Arabidopsis cDNA collection Science 296 (5565), 141-145 (2002)
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ZMMBBD0619B24r ZMMBBb (HindIII) Zea mays genomic clone ZMMBBD0619B24 3', genomic survey sequence.
                                                                                                                                                                                                                                         Email: mseki@rtc.riken.go.jp
reversed clone; Please visit our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.
Location/Qualifiers
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190 Frelinghuyeen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
                                                                                                                           Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Fax: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RAFL14"
/note="Site_1: BamHI; Site_2: Sall"

    413
    /organism="Arabidopsis thaliana"

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High quality sequence start: 116.
Location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL14-68-M24"
/tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4577"
/clone="ZMMBBb0619B24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 TAAGGGTTGATGTCCATGAC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TAAGGGUCGAUGUCCATGCC 20
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CL260820.1 GI:41624959
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Best Local Similarity 75.0%;
Matches 15; Conservative 3
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CL260820
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Nicotiana tabacum (common tobacco)

Nicotiana tabacum

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.

El (bases 1 to 457)

Matsuoka,K., Tashiro,G., Horiguchi,T., Demura,T. and Fukuda,H.

Profilling growth-phase dependent gene expression of tobacco Br-2

cells by comprehensive microarray analysis

Unpublished (2003)

Contact: Ken Mateuoka

Morphogenesis Research Group

RIKEN Plant Science Center

1-7-2 Suchirocho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Fax: 81-45-503-9573

Email: by20psc.riken.go.jp, URL:http://mrg.psc.riken.go.jp/strc/

The cDNA library was constructed from mRNA isolated from lag (9 h), log (72 h) and stationary (7 days) old Br-2 cells.

Seq primer: M13 forward.

Location/Oualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                             BP527907 BP527907 MAT001 Nicotiana tabacum cDNA clone BY12728, mRNA
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/lab_host="E. coli DH10B"
/clone lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="MAT001"
/note="Vector: pGEM-T easy; primer: M13 forward; mRNA
obtained from lag, log and stationary phase cells"
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                               431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 457;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

84.0%; Score 16.8; DB 5;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 15; Conservative 3; Mismatches 2;
                                                                                                                                      ch 84.0%; Score 16.8; DB 9;
1. Similarity 80.0%; Pred. No. 8.3e+02;
16; Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .457
/ Organism="Nicotiana tabacum"
/mol type="mRNA"
/culfivar="Bright Yellow No.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum (common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4097"
/clone="BY12728"
/cell_line="BY-2"
                                                                                                                                                                                                                                                                                     328 TAAGGGTCGATGCCCAGGCC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 TAAAGTTCGATGTCCATGCC 316
                                                                                                                                                                                                                                                      1 TAAGGGUCGAUGUCCATGCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
BP527907
BP527907.1 GI:52831634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL481016
AL481016.1 GI:11846785
GSS.
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ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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/mol_type="mkNA"
/db_xref="taxon:9606"
/clone="IMAGE:2295092"
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/tissue_type="adenocarcinoma"
/lab_host="DH108"
/clone_lib="NCI_CGAP_Pan1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BZ573222 17-DEC-2002 msh2_3006.y2 msh Pseudomonas aeruginosa genomic clone msh2_3006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG476230 1574 bp DNA linear GSS 04-JUN-2004 Mus musculus molossinus DNA, clone:MSMg01-369C21.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pecudomonadaceae; Pseudomonas.
1 (bases 1 to 773)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="msh2 3006"
/clone lib="msh"
/note="Environmental isolate. Whole genomic shotgun
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                                                                                                                                                                                                                                                                                                                Query Match

84.0%; Score 16.8; DB 1; Length 733;
Best Local Similarity 75.0%; Pred. No. 8.9e+02;
Matches 15; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Pseudomonas aeruginosa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Washington
Box 352145, Seattle, WA 98105-2145, USA
12062216954
Fax: 2066857244
Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="genomic DNA"
/strain="MSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: shotgun.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275
                                                                                                                                                                                                                                                                                                                                                                                                                                                    557 TAAGGGTCGATGTGCATGAC 576
                                                                                                                                                                                                                                                                                                                                                                                                                       1 TAAGGGUCGAUGUCCATGCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
BZ573222/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
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AG476230/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LINL at:
Insert Length: 1107 Std Brror: 0.00
Seq primer: 40UP from Gibco
High quality sequence stopp: 401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                     nhimmers ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Ball: nelsayederigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                sequencing
Campus, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 733) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                         Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajandream, M.A. and Barrell, B.G. Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hir Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
     Trypanosoma brucei
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Best Local Similarity 75.0%; Pred. No. 8.5e+02;
Matches 15; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:5691"
/clone="230d01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 TAAGGGTTGATGTCCAGGCC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TAAGGGUCGAUGUCCATGCC 20
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Homo sapiens
                                                                  rypanosoma.
L (bases 1 to 509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .509
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KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

ACCESSION VERSION

DEFINITION

RESULT 11

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AI635930

source

FEATURES

Bource

ORIGIN

PEATURES

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SOURCE

ACCESSION

VERSION KEYWORDS

REFERENCE AUTHORS TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

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/clone_libe"pocato leaves and petioles":
//clone_libe"pocato leaves and petioles:
//note="Wedctor: pBlueScript SK(-); Site 1:
//note:"Wedctor: pBlueScript SK(-); Site 2:
//note:"Wedctor: pBlueScript SK(-); Site 1:
//note:"Wedctor: pBlueScript SK(-); Site 1:
//note:"Wedctor: pBlue were supplied by Dr. Fry (Cornell University).

Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG200800 306 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-082P16.T7, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-33, Korea (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:g82-42-866-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance
The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.4; DB 2; Length 272;
Pred. No. 1.2e+03;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                            tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                           1. .272
/organiam="Solanum tuberosum"
/mol type="mRWA"
/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .306
/organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA
                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4113"
/clone="cSTB18G4"
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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AG200800.1 GI:45232975
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77.8%;
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Best Local Similarity 77.8
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S Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Birect Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Taurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail: hattori@gec.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
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EST425953 potato leaves and petioles Solanum tuberosum cDNA clone
ESTB18G4 5' sequence, mRNA sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamilds; Solanales; Solanaceae; Solanum.
1 (bases 1 to 272)
20 (bases 1 to 272)
21 (bases 1 to 272)
22 (bases 1 to 272)
23 (bases 1 to 272)
24 (bases 1 to 272)
25 (bo,J., Horshen,C.L., Doan,B., Bougri,O., Buell,C.R.,
Ronning,C.M., Fry,W.E., Tanksley,S.D. and Baker,B.
25 (beneration of Esys from potato leaves and petioles
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BAC end Sequences of Library MSMg01
Unpublished
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/clone_lib="MSMg01 Mouse Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="WSMg01-369C21.TJ"
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                           AG476230.1 GI:48183460
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Mus musculus molossinus
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Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ECORI
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R.Site 2
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FEATURES

KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

LOCUS

ACCESSION

VERSION

RESULT 14 BE922196

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Gaps

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/db xref="taxon:9598"
/clone="RP43-082P16.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN
Query Match 82.0%; Score 16.4; DB 9; Length 306;
Best Local Similarity 77.8%; Pred. No. 1.38+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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Search completed: March 17, 2005, 11:07:49 Job time : 1386.27 secs

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Title: Perfect score:

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Database

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AB163817 Hepatitis
AY254503 Hepatitis
AY50424 Hepatitis
AY274419 Hepatitis
AY274420 Hepatitis
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AY382527 Hepatitis
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1 (bases 1 to 20)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Oligonucleorides specific for hepatitis B virus
Patent: US S8564S9-A 16 05-JAN-1999;
Location/Qualifiers
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85.0%; Pred. No. 2;
ive 3; Mismatches 0;
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Sequence 16 from patent US 5856459.
AR027818
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 3 from Patent BP1072271.
AX137490 GI:14273684
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AX027819 Sequence
AX027819 Sequence
BD236992 DNA vacci
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9
AX32954 Heparitis
AX329561 Heparitis
AX329563 Heparitis
AX329563 Heparitis
AX329573 Heparitis
                                                                                                                        March 17, 2005, 04:07:57; Search time 683.733 Seconds (without alignments) 1417.372 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AR027819
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                            Biological models showing secondary disease sign and useful in developing remedies, diagnostic products and therapeutic or diagnostic procedure, method with the use of the same and cells, BD011606

DD011606

JP 2001078621-A/3.
   Selective immune down regulation (sidr) mediated transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown, J.J., Rabban, I., Donegan, J.J. and Chaudhurry, J.R.
Biological models showing secondary disease sign and useful in
developing remedies, disquestic products and therapeutic or
disquestic procedure, method with the use of the same and cells,
tissues and organs derived therefrom
Patent: JP 2001078621-A 3 27-WAR-2001,
ENZO THERAPEUTICS INC
OS Hepatitis virus (hepatitis B virus)
PN JP 2001078621-A/3
                                                                                                                                                                                                   Gaps
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/organism='Hepatitis virus (hepatitis B virus)'.
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                                                                                          /organism="Hepatitis B virus"
/mol_type="unassigned DNA"
/db_xref="taxon:10407"
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                                                                                                                                                                                                   3; Mismatches

    .21
    /organism="unidentified"
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    /db_xref="taxon:32644"

                              Patent: EP 1072271-A 3 31-JAN-2001;
ENZO THERAPEUTICS, INC. (US)
Location/Qualifiers
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Best Local Similarity 85.0%; Pred. No. 2
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14-JUL-2000 JP 2000215182
16-JUL-1999 US 09/3562?
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unclassified,
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BD011606
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RESULT 4 AR027819

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BD236992

35 bp DNA linear PAT 17-JUL-2003
DNA vaccination to cholesterol ester transfer protein in the treatment of atherosclerosis.
PAT 29-SEP-1999
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Feitelson, M. and Siracusa, L.
Transgenic animals capable of replicating hepatitis viruses and mimicking chronic hepatitis infection in humans Patent: US 6087556-A 1 11-UUL-2000;
Location/Qualifiers
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Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
Mills, J.S.
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Needleman, P. and Glenn, K.
DNA vaccination to cholesterol ester transfer protein in the treatment of atherosclerosis
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Patent: US 5856459-A 17 05-JAN-1999;
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85.0%; Pred. No. 2.1;
ive 3; Mismatches
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                                                                                                                                                                                                                                                                                               /organism="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .28
/organism="unknown"
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                Sequence 17 from patent US 5856459.
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Sequence 1 from patent US 6087556.
AR103926.1 GI:12815514
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JP 2002516656-A/17.
unidentified
                                                         AR027819.1 GI:5938639
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Best Local Similarity 85.0
Matches 17; Conservative
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ANY) SEA TO THE SEA ON THE SEA ON TO SEA ON TO SEA ON THE OBJUN-2004 DEPARTIES B VITUS ISOLATE D272811E X protein gene, partial cds, and preC/C protein gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                              translation="STTDLEAYFKDCVFKDWEELGEETRLMIFVLGGCRHKLVCAPAS"
              Sitnik, R., Rebello Pinho, J.R., Bertolini, D.A., Bernardini, A.P., Da Silva, L.C. and Carrilho, F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
                                                                                                                                                                    Direct Submission
Submitted (23-JTM-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 253)
Sitnik, R., Rebello Pinho, J.R., Bertolini, D.A., Bernardini, A.P., Silva, L.C. and Carrilho, F.J.
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Rebello Pinho, J.R., Sitnik, R., Carrilho, F.J., Da Silva, L.C. and
                                                                                                                 2 (bases 1 to 253)
Rebello Pinho, J.R., Sitnik, R., Carrilho, F.J., Da Silva, L.C.
Bernardini, A.P.
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J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
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Submitted (23-JUN-2003) Research & Development, Laboratorio
Bioquimico (ardim Paulista, Av Brig Luiz Antonio 4701, Sao E
01402-001, Brazil
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/protein id="AAQ95862.1"
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/translation="MQLFHLCLVISCTCPTFQASKLCLGWL"
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                                                                                 J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
15184419
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                                                                                                                                                                                                                                                                     /organism="Hepatitis B virus"
/mol type="genomic DNA"
/isolate="A611252E"
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/protein_id="AAQ95861.1"
/db_xref="G1:37625316"
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   (bases 1 to 253)
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Matches 17; Conservative
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AY329561/c
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                                                                                                                                                                               DNA vaccination to cholesterol ester transfer protein in the treatment of
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 35
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organism='Unidentified'
                                                                                                                                                                                                                                         Location/Qualifiers
Patent: JP 2002516656-A 17 11-JUN-2002;
                              Unidentified
Unidentified
JP 2002516556-A/17
11-JUN-2002
17-SEP-1999 UP 2000512947
19-SEP-1997 US 08/934367
PHILIP NEEDLEMAN,KEVIN GLENN
C12N15/09,A61K48/00,C12N15/00
Strandedness: Single,
                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.2;
3; Mismatches
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Patent: US 5728518-A 9 17-MAR-1998;
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/wol_type="unassigned DNA"
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192348

    .35
    /organism="unidentified"
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                                                                                                                                                                      Topology: Linear;
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Carmichael, E.
Antiviral poly-and
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Best Local Similarity
Matches 17; Conserva
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Unclassified.
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Local Similarity 85.0%; Pred. No. 2.9; ne 17; Conservative 3; Mismatches
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Submitted (13-JUN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
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Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (bases 1 to 253)
Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., I Silva,L.C. and Carrilho,F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
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Bernardini,A.P.
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85.0%; Pred. No. 2.9;
iive 3; Mismatches 0;
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                                                /codon_start=3
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Heparitis B virus isolate D296668E X protein gene, partial cds; and Av329568
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Direct Submission
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Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
Location/Qualifiers
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 253)
Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P.,
Silva,L.C. and Carrilho,F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in
Brazilian Patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 253)
Rebello Pinho,J.R., Sitnik,R., Carrilho,F.J., Da Silva,L.C. and
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Score 20;
Pred. No. 2.
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/codon start=1
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Best Local Similarity 85.0%; F
Matches 17; Conservative 3;
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Direct Submission
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CNFFTSA"
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 253)
Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., Da Silvay,L.C. and Carrilho,F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
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Direct Submission
Submitted (23-JUN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
Location/Qualifiers
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Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
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Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (bases 1 to 253)
Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P.,
Silva,L.C. and Carrilho,F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in
Brazilian Patients
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Rebello Pinho,J.R., Sitnik,R., Carrilho,F.J., Da Silva,L.C. and
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Pred. No. 2.9;
3; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 bp DNA linear VRL 08-JUN-2004 Heparitis B virus isolate D639472E X protein gene, partial cds; and AX329581
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Rebello Pinho, J.R., Sitnik, R., Carrilho, F.J., Da Silva, L.C.
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                                                                                                                                                                                                                                                                        DB 14; Length 253;
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

(Dasses 1 to 294)

Castro, L.D., Niel, C. and Gomes, S.A.

Low frequency of mutations in the core promoter and precore regions of hepatitis B virus in anti-HBe positive Brazilian carriers
BMC Microbiol. 1 (1), 10 (2001)
                                                                                                                                                                                                                           AF390000 294 bp DNA linear VRL 06-MAR-2002 Hepatitis B virus isolate D3 X protein gene, partial cds; and nonfunctional precore/core protein gene, partial sequence.
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95. .>294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 294)
De Castro,L., Niel,C. and Gomes,S.A.
Direct Submission
Submitted I.-UTM-2001) Virology, FIOCRUZ, Av. Brasil 4365, Rio de Janeiro, RJ 21045-900, Brazil
Location/Qualifiers
                                             Gaps
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Query Match 100.0%; Score 20; DB 14; Length 253; Best Local Similarity 85.0%; Pred. No. 2.9; Matches 17; Conservative 3; Mismatches 0; Indels
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Matches 17; Conservative 3; Mismatches 0; Indels (

Search completed: March 17, 2005, 08:14:18 Job time : 684.733 secs

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The present sequence represents a synthetic oligonucleotide HBV101b which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a
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Aaz98697 Human hep
Aaf58672 Hepatitis
Adb68574 NG2 A-L-P
Adb68572 A-L-P con
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Aag80499 Primer to
Aav45201 Primer MC
Aaa62585 Transgen1
Adn36070 Probe #15
Adn36071 Probe #15
Adn36071 Probe #15
Adn36072 Probe #14
Adn36065 Probe #18
Adn36067 Probe #18
Adn36065 Probe #18
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Probe #14
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Aat72576 Hepatitis
                                                                    March 17, 2005, 04:03:33 ; Search time 171.333 Seconds
  (without alignments)
  691.020 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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| Aba96791 Hepatitis | Adc64743 Hepatitis | Aax36590 PCR prime | щ | | Adj94539 HBV genom | Adr89273 Lab-on-ch | Adr89266 Lab-on-ch | Adn36055 Probe #13 | Adm41005 HBc relat | Adm41004 HBc relat | Abk67524 DNA encod | Abk67525 DNA encod | Abk67527 DNA encod | Abk67526 DNA encod | Adm40998 HBc relat | HBC | Adm41007 HBc relat | Adm41008 HBc relat | Adm41010 HBc relat | Adm41011 HBc relat | Abk44278 DNA encod | Abk67533 Immunogen | | Adg47010 Hepatitis |
|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|
| ABA96791 | ADC64743 | AAX36590 | ABX95880 | ACD07807 | ADJ94539 | ADR89273 | ADR89266 | ADN36055 | ADM41005 | ADM41004 | ABK67524 | ABK67525 | ABK67527 | ABK67526 | ADM40998 | ADM40999 | ADM41007 | ADM41008 | ADM41010 | ADM41011 | ABK44278 | ABK67533 | ADE10968 | ADG47010 |
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| 31 | 31 | 35 | 35 | 35 | 36 | 39 | 39 | 53 | 504 | 504 | 513 | 513 | 516 | 519 | 534 | 534 | 534 | 534 | 540 | 540 | 549 | 549 | 549 | 549 |
| 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| 20 | 50 | 20 | 50 | 20 | 20 | 50 | 20 | 50 | 20 | 20 | 20 | 20 | 50 | 50 | 20 | 20 | 20 | 50 | 50 | 20 | 20 | 20 | 20 | 20 |
| c 21 | C 22 | c 23 | c 24 | c 25 | c 26 | • | c 28 | c 29 | 30 | c 31 | c 32 | c 33 | c 34 | c 35 | c 36 | 37 | c 38 | 39 | c 40 | 41 | c 42 | c 43 | C 44 | c 45 |
| | | | | | | | | | | | | | | | | | | | | | | | | |

ALIGNMENTS

Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection. /*tag= a /note= "Internucleotide linkages are phosphorothioate" Mills JS; Kilkuskie RE, Hepatitis B virus RNA antisense oligonucleotide HBV101b. HBV; HBV infection; inhibition; replication; Jupp R, (HOFF) HOFFMANN LA ROCHE & CO AG F. (HYBR-) HYBRIDON INC. Location/Qualifiers Craig CJ, Frank BL, Goodchild J, Roberts NA, Roberts PC, Slade A; BP. 96WO-EP002432 95US-00467397 AAT72575 standard; DNA; 20 (first entry) NPI; 1997-043124/04.

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The present sequence represents a synthetic oligonucleotide HBV101Mb which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two noncontiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                            Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                                                       Sequence 20 BP; 5 A; 3 C; 5 G; 4 T; 3 U; 0 Other;
                                                          Claim 1; Page 12; 81pp; English
                                                                                                                                                                                    Best Local Similarity 100.
Matches 20; Conservative
            WPI; 1997-043124/04.
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08-JUL-1993
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03-APR-1992;
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note= "Internucleotide linkages are phosphorothioate"
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                                                                   100.0%; Score 20; DB 2; Length 20; 85.0%; Pred. No. 1.1; or 3; Mismatches 0; Indels
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                                                 Sequence 20 BP; 5 A; 3 C; 5 G; 7 T; 0 U; 0 Other;
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/*tag= b
/note= "2'-OMe RNA"
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Roberts NA, Roberts PC, Slade A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus; polyadenylation; targetting; cell-specific; complex;
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble mol. complex for targetting delivery of poly- or oligo-
nucleotide(s) to cells - includes carrier comprising cell-specific
binding agent and poly- or oligo-nucleotide-binding agent.
                                                                    ·.
100.0%; Score 20; DB 2; Length 20; 100.0%; Pred. No. 1.1; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense oligomer hybridising to HBV poly A site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oncogenes; pathogen; parasite; ss.
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                                                                                                                                     1 TTATAAGGGTCGAUGUCCAU 20
                                                                                                                                                                                             trataaggarcgauguccau 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-00755083.
91US-00788119.
92US-00864003.
                                                                                                                                                                                                                                                                                                                                                         AAQ38441 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-US007339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
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Hepatitis B virus; HBV; antiinflammatory; immunosuppressive; hepatchropic; virucide; vaccine; Tupaia belangeri; immune-related disoder; transplantation rejection; selective immune down regulation; SIDR; probe; se.

Hepatitis B virus. EP1072271-A2

Hepatitis B virus HB probe.

(first entry)

27-APR-2001

AAF58672;

BP.

AAF58672 standard; DNA; 21

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AAF58672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense oligonucleotides targeted to asialoglycoprotein receptor-
bearing cells useful for inhibiting viral and oncoprotein RNA expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a human hepatitis B antisense oligonucleotide which can be used as a component of the soluble molecular complex of the invention. The invention relates to a soluble molecular complex comprising a single stranded antisense oligonucleotide which hybridises to an RNA in a target cell. The antisense oligonucleotide is complexed with a carrier comprised of a ligand for the asialoglycoprotein receptor and a polycation. The molecular complex has cytostatic, virucide, hepatotrophic and anti-inflammatory activity. The complex works through cell specific antisense inhibition of RNA expression. The molecular complex is used for inhibiting oncogene and viral (especially hepatitis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA expression in asialoglycoprotein receptor-bearing cells. (Updated on 06-AUG-2003 to correct OS field.)
                             Gaps
                                                                                                                                                                                                                   Cytostatic; virucide; hepatotrophic; anti-inflammatory; antisense; hepatitis B virus; oncoprotein expression inhibitor; ss; asialoglycoprotein receptor.
                             ;
0
                                                                                                                                                                                               Human hepatitis B virus antisense oligonucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 20; DB 3; Length 21; Pred. No. 1.2; 3; Mismatches 0; Indels
        DB 2; Length 21;
                             Indels
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 5 A; 3 C; 5 G; 8 T; 0 U; 0 Other;
Score 20; DB ,
                 Pred. No. 1.2;
3; Mismatches
                                                  1 TTATAAGGGTCGAUGUCCAU 20
                                                             2 TTATAAGGGTCGATGTCCAT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Col 5; 12pp; English.
                                                                                                                          ВЪ.
                                                                                                                                                                                                                                                                                                                                               91US-00755083.
91US-00788119.
92US-00864003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
        100.08;
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                 82.0%;
                                                                                                                         21
                                                                                                                                                                           (first entry)
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Best Local Similarity 85...
Local 17; Conservative
                             17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    (UYCO-) UNIV CONNECTICUT
                                                                                                                        AAZ98697 standard; DNA;
                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-223192/19
                  Local Similarity
                                                                                                                                                                                                                                                              Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                          Wu GY;
                                                                                                                                                                                                                                                                                                                           02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                 05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                           04-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                04-SEP-1992;
                                                                                                                                                                  06-AUG-2003
                                                                                                                                                                           20-JUN-2000
                                                                                                                                                                                                                                                                                  US6030954-A
                                                                                                                                                                                                                                                                                                       29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                      03-APR-1992;
                                                                                                                                            AAZ98697;
       Query Match
Best Local
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                             Matches
                                                                                                              셤
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Native or non-native antigens, used for establishing selective immune down regulation, for transplantation, for treating or preventing undesirable immune reactions of vaccination, and for treating immune

Example 7; Page 18; 47pp; English.

disorders

Rabbani E, Ilan Y, Roy-Chowdhury J, Engelhardt DL;

WPI; 2001-170934/18

(ENZO-) ENZO THERAPEUTICS INC

17-JUL-2000; 2000EP-00115423.

31-JAN-2001

16-JUL-1999;

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The present sequence is a probe which was used in an example demonstrating disease symptoms induced in a small animal model, Tupaia demonstrating disease symptoms induced in a small animal model, Tupaia belangeri, after infection by Hepatitis B virus (HBN). This example is provided in a specification relating to the use of native or non-native antigen or antigens, or their immunological equivalent, for preparing a pharmaceutical composition for use in transplantation processes, for treating or preventing undesirable immunological consequences of vaccination or immunisation in a subject, or for treating immune-related disorders. The invention provide unique selective immune down regulation processes. They may be used for preventing or treating graft versus host rejection and for treating crown's disease, primary sclerosing cholangitis disease, primary sclerosing cholangitis disease, primary biliary cirrhosis disease, primary Celliac's disease, primary autoimmune chronic active hepatitis, chronic liver rejection disease, immune-mediated liver fibrosis disease, immune-mediated vascular disorder, and immune-mediated muscle disorders affecting smooth muscle, striated muscle and blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 5 A; 3 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TTATAAGGGTCGAUGUCCAU 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2003 (first entry)
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Matches
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Gaps

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TTATAAGGGTCGAUGUCCAU 20

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82.0%;

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The invention relates to a novel homogeneous conjugate comprising a hepatic ligand, bifunctional linker and biologically stable oligomer that binds to a sequence in a hepatic virus or pathogen and is released from the conjugate by hydrolysis or reduction. The conjugate of the invention may be useful during the treatment of liver diseases including chronic viral hepaticis, cirrhosis, malaria, viral protozoan infection and cancer, such as hepatocellular carcinoma (HCC). The current sequence is that of the A-L-P conjugate-related RNA oligomer 3 of the invention.
                                                                           homogeneous A-L-P conjugate, hepatic; chronic viral hepatitis; cirrhosis; malaria; viral infection; protozoan; cancer; hepatocellular carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New homogeneous prodrug conjugate containing hepatic ligand for delivery of pathogen-specific oligomer useful for treating liver infections or
                                                                                                                                                                                                                                                                               /note= "OTHER = 2'-O-methyl ribose alternating methyl-phosphonate-phosphodiester backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 10; Length 21; 80.0%; Pred. No. 1.2; 0; Indels iive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis B virus RNA antisense oligonucleotide HBV94b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 5 A; 3 C; 5 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ts'o POP, Duff R, Zhou Y, Deamond S,
                                       A-L-P conjugate-related RNA oligomer 3.
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 40; 107pp; English.
                                                                                                                                                                                                                                                                /mod_base= OTHER
/note= "OTHER = 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TTATAAGGGTCGAUGUCCAU 20
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                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2002; 2002WO-US019908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-2001; 2001US-00888164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT72577 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CELL-) CELL WORKS INC. (UYJO ) UNIV JOHNS HOPKINS.
04-DEC-2003 (first entry)
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                                                                                                                                                                                                                      1. .21
/*tag=
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                                                                                                                                                                                                                                                                                                                                                WO2003067209-A2
                                                                                                                                                                                                     Key
modified_base
                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                         HCC; BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hepatic ligand, bifunctional linker and biologically stable oligomer that binds to a sequence in a hepatic virus or pathogen and is released from the conjugate by hydrolysis or reduction. The conjugate of the invention may be useful during the treatment of liver diseases including chronic viral hepatitis, cirrhosis, malaria, viral or protozoan infection and cancer, such as hepatocallular carcinoma (HCC). The current sequence is that of the NG2 A-L-P conjugate DNA component of the invention which was used to target the Hepatitis B virus (HBV) c (core)-gene.
                                                    homogeneous A-L-P conjugate; hepatic; chronic viral hepatitis; cirrhosis; malaria; viral infection; protozoan; cancer; hepatocellular carcinoma; HCC; ss; NG2; HBV; c-gene; core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New homogeneous prodrug conjugate containing hepatic ligand for delivery of pathogen-specific oligomer useful for treating liver infections or cancer.
                                                                                                                                                                                                                                                                                                                                              /note= "OTHER = Optionally linked to YEE(ahGalNAc)3-SMCC and various chemical groups as shown in figures"
                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/mod_base= CTHER
/note= "CTHER = Optionally linked to chemical group as
shown in figure 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel homogeneous conjugate comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                     NG2 A-L-P conjugate DNA component used to target HBV c-gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 10; Length 21; 85.0%; Pred. No. 1.2; 0; Indels tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  'note = "OTHER = phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 5 A; 3 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roby C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deamond S,
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 83; 107pp; English.
                                                                                                                                                                                                                                             base= OTHER
                                                                                                                                                                                                                                                                                                                           /mod_base= OTHER
/note= "OTHER = (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ts'o POP, Duff R, Zhou Y,
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ADB68572
1D ADB68572 standard; RNA; 21
XX
AC ADB68572;
XX
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-697456/66
                                                                                                                                          Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003067209-A2
                                                                                                                                                                                                   modified_base
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Gaps

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HBV; HBV infection; inhibition; replication; ss.

Synthetic

BP.

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Key

Location/Qualifiers

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The present sequence represents a synthetic oligonucleotide HBV94b which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a
                                                                                                                                                                                                                                                                                                                                                     ಠ
                                                                                                                                                                                                                                                                                                                                                   sample. The antisense oligonucleotide, and oligonucleotides containing sequence which is complementary to at least two non- contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a
                                                                                                                                                                                                                                                 Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                       "Internucleotide linkages are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatitis B virus; X region; core region; primer; PCR; amplification; polymerase chain reaction; detection; viral infection; ss.
                                                                                                                                                                                     Mills JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                     Kilkuskie RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                      th 100.0%; Score 20; DB 2; Length 27; Similarity 85.0%; Pred. No. 1.2; 17; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 27 BP; 8 A; 4 C; 5 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer to amplify hepatitis B virus core region.
                                                                                                                                                                                     Jupp R,
                                                                                                                                                                                                                                                                                                                                                                                        or for the treatment of HBV infection
                                                                                                                                                (HOFF ) HOFFMANN LA ROCHE & CO AG F. (HYBR-) HYBRIDON INC.
                                                                                                                                                                                   Goodchild J,
PC, Slade A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTATAAGGGTCGAUGUCCAU 20
                                                                                                                                                                                                                                                                                        Claim 1; Page 12; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94WO-US006360.
                                                                                                  96WO-EP002432
                                                                                                                        95US-00467397
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(first entry)
                                                                                                                                                                                     Frank BL, Goo,
, Roberts PC,
1. .27
/*tag=
/note= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
AAQ80499/c
ID AAQ80499 standard; DNA;
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                                                                                                                                                                                                                          WPI; 1997-043124/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feitelson M,
                                                                                                04-JUN-1996;
                                                                                                                                                                                    Craig CJ, F:
Roberts NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-1993;
                                                                                                                        06-JUN-1995;
                                                WO9639502-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9429483-A1
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23-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ80499;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                           This primer designated MF03 covers nucleotide bases 1903-1949 at the beginning of the hepatitis B virus (HBV) core open reading frame. It is used with MF04 (AAQ80500) to amplify the core gene. The primers allow the detection of a specific class of HBV variants. They are useful for demonstrating the presence of productive virus infection and may prove useful in monitoring therapeutics. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating immune responses in mammals infected with infectious agent(s) - e.g. to reduce pathogenicity caused by immune responses in cases where the infectious agent has limited pathogenicity.
          in the X
HB X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amplification; viral infection; bacterial infection; hepatitis B virus.
                                                                                                                                                                                                                                                                                                                  Gaps
            of hepatitis B virus (HBV) variants having deletions by detection of antibodies against HBV polymerase and
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                   Score 20; DB 2; Length 28;
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                   Sequence 28 BP; 10 A; 5 C; 5 G; 8 T; 0 U; 0 Other;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      1 TTATAAGGGTCGAUGUCCAU 20
                                                                               Claim 3; Page 34; 45pp; English.
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                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                  Best_Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV45201/c
ID AAV45201 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-387782/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .mmune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9829121-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-0CT-1998
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              Detection (region - b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV45201;
                                                                                                                                                                                                                                                                                    Query Match
                                               antigen.
                                                                                                                                                                                                                   field.)
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Gaps

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Indels

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3; Mismatches

17; Conservative

Matches

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The present sequence is a PCR primer used to detect a transgene in severe combined immunodeficient (SCID) mice. Transgenic immunodeficient mice were produced that are not tolerant to hepatitis viral antigens, lack functional T-cells and contain integrated hepatitis virus blain the somatic and germ cells. The hepatitis virus gene is expressed and the hepatitis virus is replicated in the transgenic mouse. The mouse may be used as an animal model for evaluating interactions of a chemical, drug or immunomodulating agent with a hepatitis virus. It is also useful for the assessment of anti-viral and immunomodulatory intervention therapies, including the screening of drug candidates. It can be used to analyse the virus and chemicals metabolised and/or detoxified by the liver, and to identify cellular biochemical pathways contributing to the development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic mouse useful in methods for evaluating interactions of chemical, drug or immunomodulating agent with hepatitis virus, lacks functional T-cells and B-cells and is capable of replicating hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse is thus
                                                                                                                                                                                                                                                                                                       Gaps
process can modulate undesirable autoimmune responses exhibited by mammals infected with viral, bacterial and parasitic agents. It can prevent life-long disabilities which result from these infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; SCID; severe combined immunodeficiency; transgenic mouse; hepatitis virus; hepatitis B; hepatitis C; chronic liver disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to identify cellular biochemical pathways contributing to the devand progression of chronic liver disease. The transgenic mouse is useful for elucidating the effects of hepatitis virus on hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic SCID mouse hepatitis virus transgene PCR primer MF03.
                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                         100.0%; Score 20; DB 2; Length 28; 85.0%; Pred. No. 1.2; 2; ve 3; Mismatches 0; Indels
                                                                                                                                                             Sequence 28 BP; 10 A; 5 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                           1 TTATAAGGGTCGAUGUCCAU 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYJE-) UNIV JEFFERSON THOMAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA62585 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                  Local Similarity 85.0
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Siracusa L, Feitelson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-523731/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA62585;
                                                                                                                                                                                                                                Query Match
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AAA62885/c
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The invention relates to a method of predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy by determining whether the HBMS (1) bears a nucleic acid that encodes for a leucine at amino acid position (aa) 91 in the DNA polymerase region of HBW. The method comprises

(originally codon 438) or a (ii) a cysteine at aa256 (originally codon 604) in the DNA polymerase region of HBW. The method comprises

determining whether the HBV carried by the host bears one or more of the following mutations: (i) Q213S (glutamine to serine at aa213) (originally codon 604) in the HBW polymerase region, (ii) G139T, A1752C/T, T1909C, T1960G, or T1961A/G specific point mutation in the DNA precore/core promoter or open reading frame (ORF) region or (iii) a pair of nucleotide promoter or open reading frame (ORF) region or (iii) a pair of nucleotide and C1962A representing specific double point mutations in the DNA precore/core promoter or ORF region. The method and kit is useful in predicting the long-term response of a host of HBV to 3TC therapy (also known as lamivudine). This sequence represents an oligonucleotide sequence used in the method of the invention to detect a mutation in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Predicting the long-term response of a host of hepatitis B virus (HBV) to 3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.
                                                                                                                                                                                                                                             Probe #151 to determine effect of long term lamivudine treatment of HBV.
                                                                                                                                                                                                                                                                                ss; probe; hepatitis B virûs; HBV; 3TC therapy; mutation; lamivudine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28 BP; 11 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 31; SEQ ID NO 151; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TTATAAGGTCGAUGUCCAU 20
1 TTATAAGGGTCGAUGUCCAU 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 TTATAAGGGTCGATGTCCAT 4
                       20 TTATAAGGGTCGATGTCCAT 1
                                                                                                                                  ADN36070 standard; DNA; 28 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002; 2002US-0415301P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            above mentioned sequences.
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 85.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEOU ) UNIV GEORGETOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ciancio A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-348004/32.
                                                                                                                                                                                                                                                                                                                        Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                         WO2004031729-A2.
                                                                                                                                                                                                          01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                              15-APR-2004
                                                                                                                                                                       ADN36070;
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Matches
                                                                                               RESULT 12
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RESULT 13 ADN36068/c

100.0%; Score 20; DB 3; Length 28; 85.0%; Pred. No. 1.2;

Query Match Best Local Similarity

Sequence 28 BP; 10 A; S C; S G; 8 T; 0 U; 0 Other;

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Probe #149 to determine effect of long term lamivudine treatment of HBV.
                                                                                                                                                                                                                                   Predicting the long-term response of a host of hepatitis B virus (HBV) 3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.
                                                                     88; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine.
                                                                                                                                                                                                                                                                        Claim 31; SEQ ID NO 149; 107pp; English
                                                                                                                                                                                                  Gerin JL;
BP
                                                                                                                                             01-OCT-2003; 2003WO-US031121
                                                                                                                                                              01-OCT-2002; 2002US-0415301P
                                  01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 above mentioned sequences
ADN36068 standard; DNA;
                                                                                                                                                                              (GEOU ) UNIV GEORGETOWN
                                                                                                                                                                                                 Ciancio A,
                                                                                                                                                                                                                   WPI; 2004-348004/32
                                                                                       Hepatitis B virus.
                                                                                                         WO2004031729-A2
                                                                                                                           15-APR-2004
                                                                                                                                                                                                Korba BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                 ADN36068
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The invention relates to a method of predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy by determining whether the HBV carried by the host (i) bears a nucleic acid that encodes for a leucine at amino acid position (as) 91 in the DNA polymerase region (as) 10 in the DNA polymerase region of HBV. The method comprises determining whether the HBV carried by the host bears one or more of the collowing mutations: (i) Q213S (glutamine to serine at aa213) (originally codon 604) in the HBV polymerase region, (ii) G1339T, A1752CT, T1909C, T1960G, or T1961A/G specific point mutation in the DNA precore/core promoter or open reading frame (ORF) region or (iii) a pair of nucleotide and C1962A representing specific double point mutations in the DNA precore/core promoter or ORF region. The method and kit is useful in predicting the long-cerm response of a host of HBV to 3TC therapy (also known as lamivudine). This sequence represents an oligonucleotide calculation in the method of the invention to detect a mutation in the

Sequence 28 BP; 11 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

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100.0%; Score 20; DB 12; Length 28; 85.0%; Pred. No. 1.2;
                              Indels
                              ;
0
                              3; Mismatches
                                                         1 TTATAAGGGTCGAUGUCCAU 20
                                                                         25 TTATAAGGGTCGATGTCCAT
             Local Similarity 85.0
nes 17; Conservative
                              Matches
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ADN36071 standard; DNA; 28 BP.

01-JUL-2004 (first entry)

ADN36071;

Probe #152 to determine effect of long term lamivudine treatment of HBV.

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88; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine.
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Hepatitis B virus. WO2004031729-A2.

15-APR-2004

01-OCT-2003; 2003WO-US031121

01-OCT-2002; 2002US-0415301P.

(GEOU) UNIV GEORGETOWN

Gerin JL; Ciancio A, Korba BE,

WPI; 2004-348004/32.

t Predicting the long-term response of a host of hepatitis B virus (HBV) 3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.

Claim 31; SEQ ID NO 152; 107pp; English

S

above mentioned sequences.

Sequence 28 BP; 11 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Gapa ö 100.0%; Score 20; DB 12; Length 28; 85.0%; Pred. No. 1.2; Indele ö 3; Mismatches 85.0%; Query Match
Best Local Similarity 85.0
Matches 17; Conservative

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ADN36073/c ID ADN36073 standard; DNA; 28 RESULT 15

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Gaps

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ВЪ

ADN36073;

(first entry) 01-JUL-2004 Probe #154 to determine effect of long term lamivudine treatment of HBV.

ss; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine.

Hepatitis B virus.

WO2004031729-A2.

15-APR-2004

01-OCT-2003; 2003WO-US031121.

01-OCT-2002; 2002US-0415301P

(GEOU) UNIV GEORGETOWN.

Gerin JL; Ciancio A, Korba BE,

WPI; 2004-348004/32

Predicting the long-term response of a host of hepatitis B virus (HBV) to 3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.

Claim 31; SEQ ID NO 154; 107pp; English.

The invention relates to a method of predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy by determining whether the HBV carried by the host (i) bears a nucleic acid that encodes for a leucine at amino acid position (aa) 91 in the DNA polymerase region (coriginally codon 438) or a (ii) a cysteine at aa256 (originally codon 644) in the DNA polymerase region of HBV. The method comprises of the codon 604) in the HBV polymerase region, (ii) G1739T, A1752C/T, T1909C, T1960G, or T1961A/G specific point mutation in the DNA precore/core promoter or open reading frame (ORF) and A1752G, T1909G and A1911T or T1961A and C1962A representing specific double point mutations in the DNA precore/core promoter or ORF region. The method and kit is useful in precore/core promoter or ORF region. The method and kit is useful in predicting the long-term response of a host of HBV to 3TC therapy (also known as lamivudine). This sequence represents an oligonucleotide sequence used in the method of the invention to detect a mutation in the above mentioned sequences.

Sequence 28 BP; 10 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

Gaps . 0 Query Match 100.0%; Score 20; DB 12; Length 28; Best Local Similarity 85.0%; Pred. No. 1.2; Matches 17; Conservative 3; Mismatches 0; Indels

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Search completed: March 17, 2005, 06:48:44 Job time: 172.333 secs

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CD014361 211 bp mRNA linear EST 02-MAY-2003
hac3la04.x1 MPZFRikenl Danio rerio cDNA clone IMAGE:6923625 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Mashington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Hustevilla, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Ospriniformes; Oyprinidae; Danio.

1 (Dases 1 to 209)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,R., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., WashU Zebrafish EST Project 1998
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 211)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Rucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev stage="adult"
/lab_host="E. coli DH10B"
/clone lib="zebrafish adult brain"
/note="Vector: pZIPLOX; Site_1: Not1; Site_2: Sal1;
/note="Ibrary was constructed in lambdaZIPLOX. Mexcision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original
                                                                                                                                                                                                                                                                                                       Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 84.0%; Score 16.8; DB 4; Length 209; Best Local Similarity 75.0%; Pred. No. 3.5e+02; Matches 15; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "sex="mixed male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5334995"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: -40UP
High quality sequence stop: 200.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 TTATTAGGGTCGATGTGCAT 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio (zebrafish)
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Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., and Hood, L.
A sea urchin genome project: Sequence scan, virtual map, and additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
                                                                                                                                                                                                                                   AZ195485
SP 1030 Al H09 SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1030 Col=17 Row=O, genomic survey sequence.
                             Gaps
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Echinoidea, Euechinoidea, Echinacea, Echinoida,
Strongylocentrotidae, Strongylocentrotus.
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                             1; Indels
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Pred. No. 1.9e+02;
3; Mismatches 1;
  Pred. No. 55;
3; Mismatches
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California Institute of Technology
Pasadena California 91125, USA
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Location/Qualifiers
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Strongylocentrotus purpuratus
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Danio rerio (zebrafish)
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78.9%;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: (626) 395-8421
Fax: (626) 793-3047
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Best Local Similarity 78.9
Matches 15; Conservative
                        16; Conservative
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Class: BAC ends
Best Local Similarity
Matches 16; Conserv
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Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone P5912. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the Garman Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mgg.de/GABI-Rat/.
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                                                                           Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plank Mol. Biol. 53 (1-2), 247-259 (2003)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
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Weisshaar, B.
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 bp mRNA linear EST 15-yx17d02.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone 1868:261987 3', mRNA sequence.
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84.0%; Score 16.8; DB 9; Length 331;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 3; Mismatches 2; Indels
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/mol_type="genomic DNA"
/strain="Columbia 0"
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/clone="trakon:/955"
/clone="trakon:/955"
/tissue_type="intestine (2 samples) and liver (pooled)"
/lab host="DH10B (phage-resistant)"
/clone lib="mpZFRiken!"
/clone samples) and liver using
independent samples) and liver using
/clone samples) and liver (ARAGA (tag CO4):
/clone clone restriction for XXXXXX: CAAGAG (tag CO4):
/clone clone clone samples)
/clone samples)

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Arabidopsis thaliana T-DNA flanking sequence GK-876H09-026468,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              following tags substituting for XXXXXX: CAAGAG (tag COA): liver; CGGTAT (tag Cl2): intestine; and CGTATG (tag DO1): intestine. CDNA was pooled and size- selected for a 1.6 kD average insert. Library was constructed using the Cap- Trapper method as described in Genomics 2001: 77(1-2)79-90. Library donated by M. Pack, M.D. (University of Pennsylvania School of Medicine). Seq primer: T3 from Gibco.
High quality sequence stop: 211.
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Makaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis:
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Waterston, R. and Wilson, R. WashU Zebrafish EST Project 1998

Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800

Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligo-dT primed cDNA was produced from intestine (two independent samples) and liver using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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22755829
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                                                                                                                                                                                                                                                                                                                                                                                                       Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .211
/organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic survey sequence.
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Best Local Similarity
Matches 15; Conserv
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Gaps

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LOCUS DEFINITION CR405240/c

RESULT 5

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ORIGIN

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE

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Email: zbrafish@watson.wustl.edu
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                                                                                                                                                                                                                                  /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0
Matches 15; Conservative
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BI840986
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KEYWORDS
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1 (Dases 1 to 426)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Waterston,R. and Wilson,R.
WashU Zebrafish EST Project 1998
                                                             Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 237
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 237.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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fx05f04.x1 Gong zebrafish ovary Danio rerio cDNA clone
IMAGE:5619198 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.8; DB 7; Length 420; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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75.0%; Pred. No. s.c.
                                                                                                                                                                                                                                                                     1. .420
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="GDB:3871629"
/db_xref="taxon:9606"
/clone="IMAGE:261987"
              The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 TTCTCAGGGTCGATGTCCAT 113
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BM571757.1 GI:18853740
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                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15, Conservative
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Best Local Similarity
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Wilson, R
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SOURCE
ORGANISM
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JOURNAL
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BM571757
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                                               COMMENT
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lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo mass-excised to pBluescript SK- following the Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="4-5 month"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lone_lib="Gong zebrafish ovary"
/note="Organ: ovary (pooled); Vector: pBluescript SK-;
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
cDNAs were and oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on this library (National University of Singapore, Department of Balological Sciences, Lower Kent Ridge Road, Singapore 119260)."
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1 (Dases 1 to 433)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theison, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish EST Project 1998
Unpublished (1998)
The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).

Seq primer: T7 from Gibco.

Location/Qualifiers
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cDNA Library Arrayed by:
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
T=1: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                       /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5619198"
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H98688
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KEYWORDS
SOURCE
ORGANISM
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H98688
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JOURNAL
COMMENT
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Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L.,

Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y.,

Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,

Washu Kenopus Est project, 1999

Unpublished (1999)
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WashU Xenopus EST project, 1999
Washington University School of Medicine
Mashington University School of Medicine
A444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
EAX: 314 286 1810
Fax: 314 286 1810
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dal3f06.yl normalized Xenopus laevis gastrula Xenopus laevis CDNA clone XENOPUS_SOURCE_ID:xInga001c12 5' similar to SW:AOP2_HUMAN P30041 ANTIOXIDANT PROTEIN 2 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                Mass
                                                                                                                                                                                                                                                                                                            /dev stage="adult"
/lab_host="E. coli DH10B"
/clone lib="xebratish adult brain"
/clone lib="xebratish adult brain"
/clone lib="xebratish adult brain"
/criginal library was constructed in lambdaZIPLOX. Mexcision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XENOPUS_SOURCE_ID:xlnga001c12"
/tissue_type="gastrula_(stages 10.5, 11.5 mixed)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.0%; Score 16.8; DB 4; Length 433; 75.0%; Pred. No. 3.9e+02; ive 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                               /clone="IMAGE:4833939"
/sex="mixed male and female"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: -40RP from Gibco
High quality sequence stop: 385.
Location/Qualifiers
                                                                                                                                                                               /organism="Danio rerio"
                                                                                       Seg primer: -40UP
High quality sequence stop: 396.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 bp
                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.09
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library
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AW147602/c
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/dione libe-normalized Xenopus laevis gastrula"
/dione libe-normalized Xenopus laevis gastrula"
/note="Vector: pBluescript SK-; Site 1: ECORI; Site 2:
Xho1; CDNA was prepared from 2ug of poly A+ RNA (equal parts from stage 10.5 and stage 11.5 gastrulae).
ECORI-XhoI cut CDNA was then ligated into Unizap-XR (Stratagene) with ECORI at the 5' end and XhoI at the 3' end. SS-library phagemids were prepared by mass excision from the original library and normalized by hybridization to bictinylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Cho et al. 1991 Cell 67, 1111-1120). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished). Note: This is a Xenopus Gene Collection (XGC) library."
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
High quality sequence stops: 324
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: and 3-40 forward
High quality sequence stop: 324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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yx17h02.81 Soares melanocyte 2NbHM Homo sapiens cDNA clone
H9868B
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/lab_howit="DH10B (ampicillin resistant)"
/clone lib="Soares melanocyte 2NDHM"
/note="Vector: pT7T3D (Pharmacia) with a modified
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%; Score 16.8; DB 2; Length 438; 75.0%; Pred. No. 3.9e+02; ive 3; Mismatches 2; Indels (
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/db_xref="GDB:3871677"
/db_xref="taxon:9606"
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The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 TTATAAGAGTTGATGTCCAT 280
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Homo sapiens
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Matches 15; Conservative
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ORIGIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (Jases 1 to 477)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., WashU Zebrafish EST Project 1998

Unpublished (1998)

Unpublished (1998)

Unpublished (1998)

Unter ESTs: fx05f04.x1

Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Fax: 144 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 144 Edge 1800
BM571990 477 bp mRNA linear EST 21-FEB-2002 Ex05f04.yl Gong zebrafish ovary Danio rerio cDNA clone IMAGE:5619198 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stommer="4-5 month"

/dev_stommer="4-5 month"
/lab host="bH108 (phage-resistant)"
/clone lib="Gong zebrafish ovary"
/note="Organ: ovary (pooled); Vector: pBluescript SK-;
/sto="Organ: ovary (pooled); Vector: pBluescript SK-;
/sto="I Xh01; Site 2: EcoR1; Poly At RNA was isolated from the ovaries of 2 female adult zebrafish (4-5 month old).
CDNAs were made using oligo-dT primers and inserted into mass-excised to pBluescript SK- following the Washington University protocol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: zbrafish@watson.wustl.edu
The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Seq primer: T3 ET from Amersham
High quality sequence stop: 394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5619198"
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BM571990.1 GI:18853977
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                                                                                                                                                                                                                                                                                                                                            15; Conservative
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(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."
                                                                                                                                                                                                                                                                                                                     BW093445
BW093445 Nori Satoh unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone rcitb046h04 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone lib="Nori Satoh unpublished cDNA library, tailbud
embryo"
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes; Cyprinidae, Danio.
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                                                                                                                     ch 84.0%; Score 16.8; DB 4; Length 477; Similarity 75.0%; Pred. No. 3.9e+02; 15; Conservative 3; Mismatches 2; Indels (
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75.0%; Pred. No. 3.9e+02;
iive 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Ciona intestinalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |mol_type="mRNA"
|db_xref="taxon:7719"
|clone="rcitb046h04"
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BW093445.1 GI:24269247
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Danio rerio (zebrafish)
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Department of Zoology
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BW093445/c
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Conservative
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Best Local Similarity
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AUTHORS
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E 1 (bases 1 to 508)

S clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Washu Zebrafish EST Project 1998

L Unpublished (1998)

Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BW234048 528 bp mRNA linear BST 07-NOV-2002
BW234048 Nori Satch unpublished cDNA library, tailbud embryo Ciona
intestinalis cDNA clone citb046h04 5', mRNA sequence.
BW234048
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1 (bases 1 to 528)
53ctou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
Contact: Nori Satoh
Department of Zoology
Kyoto University
                                                                                                                                                                                                                                                                                               Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: John Ngai. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
www.zpd.de)
Seq primer: -40UP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="mixed male and female"
/tissue type="brain"
/dev_stage="abult"
/lab_host="E. coli DH10B"
/clone_lib="zebrafish adult brain"
/note="vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
/notes="vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
/notes="vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
/original library was constructed in lambdaZIPLOX.
excision of the cDNA library was performed to yield
pZIPLOX plasmids. Insert check was done in original
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Tel: 81-75-753-4081
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/organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 444. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5386027"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 TTATTAGGGTCGATGTGCAT 199
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Best Local Similarity 75.v
a 15; Conservative
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BW234'048
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BW392185 Yutaka Satou unpublished cDNA library, embryo whole animal Ciona intestinalis cDNA clone ciem807010 3', mRNA sequence.
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/dev_stage="embryo"
/clone_lib="Yutaka Satou unpublished cDNA library, embryo
whole animal"
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Bukaryota, Metazoa; Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia; Cionidae; Ciona.
I (bases 1 to 551)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2004)
Unpublished (2004)
                                                                                                                                                      /tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud
embryo"
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Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
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س
                                                                     /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb046h04"
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75.0%; Pred. No. 4e..
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/db_xref="taxon:7719"
/clone="ciem807010"
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                                       Location/Qualifiers
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Best Local Similarity 75.0
Matches 15; Conservative
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Run on:

Sequence:

Searched:

Database

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AY274420 Hepatitis
AY274424 Hepatitis
AY274424 Hepatitis
AY274424 Hepatitis
AY274439 Hepatitis
AY274431 Hepatitis
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Unclassified.
1 (lassified.
1 (bases 1 to 27)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J. Charles. and
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Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 bp
Sequence 17 from patent US 5856459.
AR027819
AR027819.1 GI:5938639
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 19 from patent US 5856459.
AR027821
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AY382523
AY382524
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Mills,J.S.
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AR027819 Sequence
BA23692 DNA vacci
192348 Sequence
BA32859 Hepatitis
AY329561 Hepatitis
AY329573 Hepatitis
AB167673 Hepatitis
                                                                                       March 17, 2005, 04:07:57 ; Search time 683.733 Seconds
   (without alignments)
1417.372 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                             9416466
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                  4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                nucleic search, using sw model
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AY329562
AY329573
AY329575
AY329575
AY329581
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AR027819
AR103926
BD236992
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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PAT 29-SEP-1999

PAT 29-SEP-1999

REFERENCE AUTHORS

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Gaps

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PAT 01-DEC-1998

linear

Query Match

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FEATURES

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AR103926/c
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ORGANISM

KEYWORDS

AUTHORS TITLE

JOURNAL

FEATURES

ORIGIN

REFERENCE

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Heperitis B virus isolate A611252E X protein gene, partial cds; and A7329529
Topology: Linear;
DNA vaccination to cholesterol ester transfer protein in the
treatment of
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 253)
Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., Blara, Lis B virus Gency, S virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 20; DB.6; Length 81;
Pred. No. 1.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Length 35;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 20; DB 6; Length 35
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 1; Mismatches 0; Indels
                                                                                                                                    J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
                                                                                                               Location/Qualifiers
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Patent: US 5728518-A 9 17-MAR-1998;
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/wol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192348 81 bp
Sequence 9 from patent US 5728518.
                                                                                                                                                                                                                          1. .35
/organism="unidentified"
                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db xref="taxon:32644"
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95.0%; P
                                                                                      atherosclerosis
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Carmichael, E.
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Best Local Similarity 95.04
Matches 19; Conservative
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AY329529/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 28)
Feitelson, M. and Siracusa, L.
Transgenic animals capable of replicating hepatitis viruses and mimicking chronic hepatitis infection in humans
Patent: US 6087556-A 1 11-JUL-2000;
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Needleman, P. and Glenn, K.
DNA vaccination to cholesterol ester transfer protein in the treatment of atherosclerosis
Patent: JP 2002516656-A 17 11-JUN-2002;
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100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 1; Mismatches 0; Indels
Mills,J.S.
Oligonucleotides specific for hepatitis B virus
Patent: US 5856459-A 17 05-JAN-1999;
Location/Qualifiers
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OS Unidentified
PN 4D 2002516656-A/17
PD 11-UUN-2002
PF 17-SEP-1998 JP 2000512947
PR 19-SEP-1997 US 08/934367
PI PHILIP NEEDLEMAN, KEVIN GLENN
PC C12N15/09, A61K48/00, C12N15/00
CC Strandedness: Single;
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Sequence 1 from patent US 6087556.
AR103926.1 GI:12815514
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Matches 19; Conserva
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RESULT 4 BD236992/c LOCUS DEFINITION

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VERSION KEYWORDS SOURCE ORGANISM

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AY329568/c
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AY329562/c
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CNFFTSA"
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Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
Viruses, Berroid viruses, Hepadnaviridae, Orthohepadnavirus.

1 (bases 1 to 253)
Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., Da Silva,L.C. and Carrilho,F.J.

Silva,L.C. and Carrilho,P.J.

Brazilian Patients
J. Clin, Microbiol. 42 (6), 2455-2460 (2004)
Direct Submission
Submitted (23-JUN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUN-2003) Research & Development, Laboratorio Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo 01402-001, Brazil
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Rebello Pinho J.R., Sitnik,R., Carrilho,F.J., Da Silva,L.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Score 20; DB
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 1; Mismatches
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KEYWORDS
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AY329562 253 bp DNA linear VRL 08-JUN-2004 Hepatitis B virus isolate D273984E X protein gene, partial cds; and preC/C protein gene, complete cds.
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 253)
Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., Islay,L.C. and Carrilho,F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in
Brazilian Patients
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Submitted (23-JUN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
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Rebello Pinho,J.R., Sitnik,R., Carrilho,F.J., Da Silva,L.C. and
Bernardini,A.P.
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Location/Qualifiers
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/mol_type="genomic DNA"
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                                                                                                                                                   100.0%; Score 20; DE
llarity 95.0%; Pred. No. 89;
Conservative 1; Mismatches
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Best Local Similarity 95.0%; F
Matches 19; Conservative 1;
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translation="STTDLEAYFKDCLFKDWEELGEEIRLKVFVLGGCRHKLVCAPAS"
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Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P., Da Sitnik,L.C. and Carrilho,F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
                                       Direct Submission
Submitted (23-JUN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
Location/Qualifiers
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Best Local Similarity 95.0
Matches 19; Conservative
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Direct Submission
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253 bp DNA linear VRL 08-JUN-2004
Hepatitis B virus isolate D296668E X protein gene, partial cds; and AY329568
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CNFFTSA"
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                                                                                                                         Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

1 (bases 1 to 253)
Sitnik, R., Rebello Pinho, J.R., Bertolini, D.A., Bernardini, A.P., Da Silva, L.C. and Carrilho, F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
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I (base) 1 to 253
Sitnik R., Rebello Pinho, J.R., Bertolini, D.A., Bernardini, A.P., Da Silva, L.C. and Carrilho, F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in Brazilian Patients
J. Clin. Microbiol. 42 (6), 2455-2460 (2004)
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Submitted (13-UN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
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Rebello Pinho,J.R., Sitnik,R., Carrilho,F.J., Da Silva,L.C. and
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Rebello Pinho,J.R., Sitnik,R., Carrilho,F.J., Da Silva,L.C.
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/translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
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ilarity 95.0%; Pred. No. 89;
Conservative 1; Mismatches
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Hepatitis B virus
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Best Local Similarity
Matches 19; Conserval
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Hepatitis B virus precore and core protein gene, 5' end of cds. L12359. L12359.1 GI:306267
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Hepatitis B virus
Viruses, Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 234)
Castro, L.D., Niel, C. and Gomes, S.A.
Low frequency of mutations in the core promoter and precore regions of hepatitis B virus in anti-HBe positive Brazilian carriers
BMC Microbiol. 1 (1), 10 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tong, S.P., Li, J.S., Vitvitski, L. and Trepo, C. Active hepatitis B virus replication in the presence of anti-HBe is associated with viral variants containing an inactive pre-C region Virology 176 (2), 596-603 (1990)
            AF390000 294 bp DNA linear VRL 06-MAR-2002 Hepatitis B virus isolate D3 X protein gene, partial cds; and nonfunctional precore/core protein gene, partial sequence.
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Li,J.S., Tong,S.P., Wen,Y.M., Vitvitski,L., Zhang,Q. and Trepo,C.
Hepatitis B virus genotype A rarely circulates as an HBe-minus
mutant: possible contribution of a single nucleotide in the precore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95. .>294
/note="nonfunctional precore/core protein due to mutation"
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De Castro,L., Niel,C. and Gomes,S.A.
Direct Submission
Submitted (11-JUN-2001) Virology, FIOCRUZ, Av. Brasil 4365, Rio de Janeiro, RJ 21045-900, Brazil
Location/Qualifiers
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Hepatitis B virus
Hepatitis B virus
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    .294
    forganism="Hepatitis B virus"
/mol type="genomic DNA"
/isolate="D3"

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Best Local Similarity 95.0
Matches 19; Conservative
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HPBHBED/c
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| Ab xref="GI:3762541"
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Submitted (23-JUN-2003) Research & Development, Laboratorio
Bioquimico Jardim Paulista, Av Brig Luiz Antonio 4701, Sao Paulo
01402-001, Brazil
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Sitnik,R., Rebello Pinho,J.R., Bertolini,D.A., Bernardini,A.P.,
Silva,L.C. and Carrilho,F.J.
Hepatitis B Virus Genotypes and Precore and Core Mutants in
Brazilian Patients
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/translation="MQLFHLCLIISCSCPTVQASKLCLGWL"
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/organiam="Hepatitis B virus"
/mol type="genomic DNA"
/isolate="D639472E"
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95.0%; Pred. No. 89;
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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

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Tanaka,Y., Hasegawa,I., Kato,T., Orito,E. and Mizokami,M.
A Case-control Study for Differences among Hepatitis B Virus
Infections of Genotypes A (Subtypes Aa and Ae) and D
Unpublished
L Unpublished
L Chases I to 398)
S Tanaka,Y. and Mizokami,M.
Direct Submission
Submitted (15-MAR-2004) Yasuhito Tanaka, Nagoya City University
Graduate School of Medical Sciences, Department of Clinical
Molecular Informative Medicine; I Kawasumi, Mizuho-cho, Mizuho-ku,
Nagoya, Aichi 467-8601, Japan (E-mail:ytanaka@med.nagoya-cu.ac.jp,
Tel:81-52-853-8292, Fax:81-52-842-0021)
                                                                                                                                                                                                                                                                                                                                        /proteIn_id="AAB03102.1"
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PEHCSHHHTALRQAILCWGELMTLATWVGANLDDPASR"
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/note="precore-core region"
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/product="polyprotein"
/protein id="BAD52175.1"
/db xref="fg1:53148167"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB167603 398 bp DNA linear VRL 01-OCT-2004 Hepatitis B virus gene for polyprotein, partial cds, clone: NEP75. AB167603.1 GI:53148166
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/mol_type="genomic DNA"
/mol_type="genotype D; from French HBeAg- patient"
/note="genotype D; from French HBeAg- patient"
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/mol_type="genomic DNA"
/db Xref="taxon:10407"
/clone="NEP75"
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82. .84
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Location/Qualifiers
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Matches 19; Conservative
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AUTHORS
TITLE
JOURNAL
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1 AAATTCTTTATAAGGGUCGA 20
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Search completed: March 17, 2005, 08:14:18 Job time : 683.733 secs

HBV Hbc-C HBV Hbc-C PCR prime PCR prime

PCR prime Influenza Recombina

Influenza Probe #13 Chimeric

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Title: Perfect score:

Sequence:

nucleic

Run on:

Adp73665 HBV PKK-2
Adp73667 HBV PKK-2
Adr12912 HBV Hbc-C
Adg46976 PCR prime
Adm81321 PCR prime
Adm81229 Influenza
Adg77004 PCR prime
Adg77005 PCR prime

Influenza

PCR prime Influenza Recombina Influenza Influenza HBc relat

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The present sequence represents a synthetic oligonucleotide HBV93b which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a
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/note= "Internucleotide linkages are phosphorothioate"
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ADG64056
ADG64056
ADP73665
ADP73667
ADR12912
ADR12912
ADG46976
ADG46976
ADG47004
ADG47004
ADG47004
ADG47004
ADG4129
ADG73782
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/*tag= a
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  AAT72579 standard; DNA; 20
 WPI; 1997-043124/04.
04-JUN-1996;
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  Synthetic
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  Aat7259 Hepatitis
Aat7257 Hepatitis
Aag0439 Frimer to
Aav45201 Primer to
Aav45201 Primer to
Aav45201 Primer to
Adn36074 Probe #15
Adn36073 Probe #15
Adn36077 Probe #15
Adn36077 Probe #15
Adn36077 Probe #15
Adn36079 Probe #15
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                                                                                March 17, 2005, 04:03:33 ; Search time 171.333 Seconde (without alignments) 691.020 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                             nucleic search, using sw model
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AAT72580
AAT72580
AAC80499
AAV45201
AAA62585
ADN36074
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Gapop 10.0 , Gapext 1.0
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geneseqn2003bs:*
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The present sequence represents a synthetic oligonucleotide HBV93Mb which is complementary to a portion of the hepstilis B virus (HBN) RM. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non-contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
  Claim 1; Page 12; 81pp; English.
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'note= "Internucleotide linkages are phosphorothioate"
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                                                                 DB 2; Length 20;
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                                              Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
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/mod_base= OTHER
/note= "2'-O-methyladenosine"
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                                                          100.0%; Score 20; I
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/note= "2'-OMe RNA"
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Roberts PC, Slade A;
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Matches 19; Conservative
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Roberts NA,
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Sequence 20 BP; 7 A; 2 C; 4 G; 6 T; 1 U; 0 Other;
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immune response; hepatitis B virus.
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                                      Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA62585/c
ID AAA6756
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This primer designated MF03 covers nucleotide bases 1903-1949 at the beginning of the hepatitis B virus (HBV) core open reading frame. It is used with MF04 (AAQ080500) to amplify the core gene. The primers allow the detection of a specific class of HBV variants. They are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         demonstrating the presence of productive virus infection and may prove useful in monitoring therapeutics. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ×
                                                                                                                                                                                                                                                                                                                              hepatitis B virus; X region; core region; primer; PCR; amplification; polymerase chain reaction; detection; viral infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88; PCR; primer; amplification; viral infection; bacterial infection;
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of hepatitis B virus (HBV) variants having deletions in region - by detection of antibodies against HBV polymerase and HB
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0; Indels
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                                                                                                                                                                                                                                                                                             Primer to amplify hepatitis B virus core region.
 Mismatches
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                                    1 AAATTCTTTATAAGGGUCGA 20
                                                       1 AAATTCTTTATAAGGGTCGA 20
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                                                                                                                                                                AAQ80499 standard; DNA; 28 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYJE-) UNIV JEFFERSON THOMAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guo J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
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Best Local Similarity 95.0%;
                                                                                                                                                                                                                                       (revised)
(first entry)
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 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peitelson M, Duan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-036505/05.
                                                                                                                                                                                                                                                                                                                                                                                                                           WO9429483-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-1994;
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                                                                                                                                                                                                                                     25-MAR-2003
23-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                   AAQ80499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen.
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                                                                                                                          RESULT 4
AA080499/c
DD AA0804
XX AA0804
DT 25-MAR
XX MW9429
XX MW91, 1
XX M
Matches
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The primers AAV45201 and AAV45202 were used to detect the presence of a HBV genome which had been microinjected into embryos of SCID mice in an example to demonstrate modulating an immune response in a mammal infected with an infectious agent. This comprises transmucosal administration of a composition comprising an epitope which is located in close proximity to the immune response. The process may be used in treatment of mammals which are acutely or chronically infected with infectious agents, such as viruses or bacteria. It may be used to increase the immune response, or it may be used to decrease the immune response in cases where the infectious agent itself exhibits limited pathogenicity but the immune response to the infectious agent causes more significant pathogenicity. This can be the case in, e.g. hepatitis B virus (HBV) infection. The process can modulate undesirable autoimmune responses exhibited by mammals infected with viral, bacterial and parasitic agents. It can prevent life-long disabilities which result from these infections
                                                                                                                                                                                                                                                                                                                                    Modulating immune responses in mammals infected with infectious agent(s) - e.g. to reduce pathogenicity caused by immune responses in cases where the infectious agent has limited pathogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic SCID mouse hepatitis virus transgene PCR primer MF03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 20; DB 2; Length 28; 95.0%; Pred. No. 7.1; 0; Indels ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28 BP; 10 A; 5 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 37; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAATTCTTTATAAGGGUCGA 20
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                                                                                      UYJE- ) UNIV JEFFERSON THOMAS
97US-0034596P.
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hes 19; Conservative
                                                                                                                                                                        Block T;
                                                                                                                                                                                                                                                          WPI; 1998-387782/33.
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    02-JAN-1997;
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combined immunodeficient (SCID) mice. Transgenic immunodeficient mice were produced that are not tolerant to hepatitis viral antigens, lack functional T-cells and B-cells and contain integrated hepatitis virus latter in the somatic and germ cells. The hepatitis virus gene is expressed and the hepatitis virus is replicated in the transgenic mouse. The mouse may be used as an animal model for evaluating interactions of a chemical, drug or immunomodulating agent with a hepatitis virus. It is also useful the assessment of anti-viral and immunomodulatory intervention therapies, including the screening of drug candidates. It can be used to analyse the virus and chemicals metabolised and/or decoxified by the liver, and to identify cellular biochemical pathways contributing to the development and progression of chronic liver disease. The transgenic mouse is thus useful for elucidating the effects of hepatitis virus on hepatic
                                                                                                                                                                                                                                                                                                                                                    present sequence is a PCR primer used to detect a transgene in severe
                                                                                                                                                                                    Transgenic mouse useful in methods for evaluating interactions of chemical, drug or immunomodulating agent with hepatitis virus, lacks functional T-cells and B-cells and is capable of replicating hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28 BP; 10 A; 5 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                      Example 3; Col 8; 7pp; English.
                                           (UYJE-) UNIV JEFFERSON THOMAS
96US-00641803
                                                                                          Feitelson M;
                                                                                                                                     WPI; 2000-523731/47
02-MAY-1996;
                                                                                          Siracusa L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metabolism
                                                                                                                                                                                                                                                          viruses
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Score 20; DB 3; Length 28; Pred. No. 7.1; 1; Mismatches 100.0%; 95.0%; P 19; Conservative Query Match Best Local Similarity Best Loc Matches 셤 ઠે

ADN36074 standard; DNA; 28 BP

to determine effect of long term lamivudine treatment of HBV. (first entry) 01-JUL-2004 Probe #155 ADN36074;

88; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine. 01-OCT-2003; 2003WO-US031121 Hepatitis B virus. WO2004031729-A2. 15-APR-2004

Gerin JL; (GEOU) UNIV GEORGETOWN Ciancio A, Korba BE,

01-OCT-2002; 2002US-0415301P

WPI; 2004-348004/32

Predicting the long-term response of a host of hepatitis B virus (HBV) 3TC therapy comprises determining whether the HBV bears a nucleic acid

t C

leucine at amino acid position (as) 91 in the DNA polymerase region (criginally codon 438) or a (ii) a cysteine at aa256 (originally codon 604) in the DNA polymerase region of HBV. The method comprises determining whether the HBV carried by the host bears one or more of the following mutations: (i) Q2138 (glutamine to serine at aa213) (originally codon 604) in the HBV polymerase region, (ii) G1739T, A1752C/T, T1909C, T1960A, or T1961A/G specific point mutation in the DNA precore/core promoter or open reading frame (ORF) region or (iii) a pair of nucleotide changes A1738C and G1739T, A1750G and A1752G, T1909G and A191T or T1961A and G1962A representing specific double point mutations in the DNA precore/core promoter or ORF region. The method and kit is useful in predicting the long-term response of a host of HBV to 3TC therapy (also known as lamivudine). This sequence represents an oligonucleotide sequence used in the method of the invention to detect a mutation in the The invention relates to a method of predicting the long term response ca host of hepatitis B virus (HBV) to 3TC therapy by determining whether the HBV carried by the host (i) bears a nucleic acid that encodes for a encoding leucine at amino acid position (aa) 91 or cysteine at aa256 Claim 31; SEQ ID NO 155; 107pp; English above mentioned sequences.

Sequence 28 BP; 9 A; 5 C; 6 G; 8 T; 0 U; 0 Other;

Gaps ., Score 20; DB 12; Length 28; Pred. No. 7.1; Indels ; 0 1; Mismatches Pred. No. 1 AAATTCTTTATAAGGGUCGA 20 100.0%; 95.0%; P Query Match 100. Best Local Similarity 95.0 Matches 19; Conservative ò

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7 26 AAATTCTTTATAAGGGTCGA BP. ADN36080 standard; DNA; 28 ADN36080; g

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Gaps

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0; Indels

01-JUL-2004 (first entry)

Probe #161 to determine effect of long term lamivudine treatment of HBV. ss; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine.

Hepatitis B virus.

WO2004031729-A2.

01-OCT-2003; 2003WO-US031121.

15-APR-2004.

01-OCT-2002; 2002US-0415301P.

(GEOU) UNIV GEORGETOWN

Gerin JL; Ciancio A, Korba BE,

WPI; 2004-348004/32.

S Predicting the long-term response of a host of hepatitis B virus (HBV) 3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.

Claim 31; SEQ ID NO 161; 107pp; English

οĘ The invention relates to a method of predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy by determining whether the HBV carried by the host (i) bears a nucleic acid that encodes for a leucine at amino acid position (aa) 91 in the DNA polymerase region (originally codon 438) or a (ii) a cysteine at aa256 (originally codon S

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determining whether the HBV carried by the host bears one or more of the Collowing mutations: (i) Q213S (glutamine to serine at aa213) (originally collowing mutations: (i) Q213S (glutamine to serine at aa213) (originally codon 604) in the HBV polymerase region, (ii) G1739T, A1752C/T, T1909C, T1960G, or T1961A/G specific point mutation in the DNA precore/core promoter or open reading frame (ORF) region or (iii) a pair of nucleotide changes A1738C and G173PT, A175CG, T1909G and A191T or T1961A and C1962A representing specific double point mutations in the DNA precore/core promoter or ORF region. The method and kit is useful in predicting the long-term response of a host of HBV to 3TC therapy (also known as lamivudine). This sequence represents an oligonucleotide sequence used in the method of the invention to detect a mutation in the above mentioned sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28 BP; 8 A; 6 C; 5 G; 9 T; 0 U; 0 Other;
          88888888888888888888888888
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100.0%; Score 20; DB 12; Length 28; 95.0%; Pred. No. 7.1; 0; Indels Pred. No. Query Match

1; Mismatches 1 AAATTCTTTATAAGGGUCGA 20 20 AAATTCTTTATAAGGGTCGA 1 19; Conservative Best Local Similarity Matches 8

ADN36073 standard; DNA; 28 BP ADN36073;

01-JUL-2004 (first entry)

Probe #154 to determine effect of long term lamivudine treatment of HBV.

ss; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine.

Hepatitis B virus.

WO2004031729-A2.

15-APR-2004

01-OCT-2003; 2003WO-US031121.

01-OCT-2002; 2002US-0415301P.

(GEOU) UNIV GEORGETOWN

Gerin JL; Ciancio A, Korba BE,

WPI; 2004-348004/32.

Predicting the long-term response of a host of hepatitis B virus (HBV) to 3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.

Claim 31; SEQ ID NO 154; 107pp; English.

The invention relates to a method of predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy by determining whether the HBV carried by the host (i) beass a nucleic acid that encodes for a leucine at amino acid position (as) 91 in the DNA polymerase region (originally codon 438) or a (ii) a cysteine at aa256 (originally codon 604) in the DNA polymerase region of HBV. The method comprises determining whether the HBV carried by the host bears one or more of the following mutations: (i) Q2135 (glutamine to serine at aa213) (originally codon 604) in the HBV polymerase region, (ii) G1739T, A172c/T, T1909C, T1960G, or T1961A/G specific point mutation in the DNA precore/core promoter or open reading frame (ORF) region or (iii) a pair of nucleotide changes A1738C and G1739T, A175C, T1909C and G173PT, A175C, T1909C and G175C, T1905C and A175CG and A175CC and A175C

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predicting the long-term response of a host of HBV to 3TC therapy (also known as lamivudine). This sequence represents an oligonucleotide sequence used in the method of the invention to detect a mutation in the
                                                                               above mentioned sequences
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Seguence 28 BP; 10 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 20; DB 12; Length 28; 95.0%; Pred. No. 7.1; cive 1; Mismatches 0; Indels Query Match
Best Local Similarity 95.0'

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RESULT 10 ADN36075/

BP. ADN36075 standard; DNA; 28

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Gaps

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ADN36075;

01-JUL-2004

Probe #156 to determine effect of long term lamivudine treatment of HBV.

38; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine.

Hepatitis B virus.

WO2004031729-A2

15-APR-2004

01-OCT-2003; 2003WO-US031121

01-OCT-2002; 2002US-0415301P.

(GEOU) UNIV GEORGETOWN

Ciancio A, Korba BE,

WPI; 2004-348004/32.

S Predicting the long-term response of a host of hepatitis B virus (HBV) 3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.

Claim 31; SEQ ID NO 156; 107pp; English

The invention relates to a method of predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy by determining whether the HBV carried by the host (i) bears a nucleic acid that encodes for a leucine at amino acid position (as) 91 in the DNA polymerse region (criginally codon 438) or a (ii) a cysteine at aa256 (originally codon 604) in the DNA polymerse region of HBV. The method comprises equion of the cermining whether the HBV carried by the host bears one or more of the following mutations: (i) Q2135 (glutamine to serine at aa213) (originally codon 604) in the HBV polymerse region, (ii) G17397, A1752C/T, T1999C, T1960G, or T1961AG specific point mutation in the DNA precore/core promoter or open reading frame (ORF) region or (iii) a pair of nucleotide changes A1738C and G13397, A1750G and A1752C, T199G and A1911T or T1961A precore/core promoter or ORF region. The method and kit is useful in precore/core promoter or ORF region. The method and kit is useful in sequence used in the method of the invention to detect a mutation in the above mentioned sequences.

Sequence 28 BP; 10 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

100.0%; Score 20; DB 12; Length 28; 95.0%; Pred. No. 7.1; Best Local Similarity Query Match

Probe #158 to determine effect of long term lamivudine treatment of HBV.

(first entry)

01-JUL-2004

ADN36077;

ss; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine.

Hepatitis B virus. WO2004031729-A2.

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ADN36077 standard; DNA; 28 BP.

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The invention relates to a method of predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy by determining whether the HBV carried by the host (i) bears a nucleic acid that encodes for a leucine at amino acid position (a) 31 in the DNA polymerase region (originally codon 438) or a (ii) a cysteine at aa256 (originally codon 604) in the DNA polymerase region of HBV. The method comprises determining whether the HBV carried by the host bears one or more of the following mutations: (i) Q213S (glutamine to serine at aa213) (originally codon 604) in the HBV polymerase region, (ii) G173F, A175C/T, T199C, T1960G, or T1961A/G specific point mutation in the DNA precore/core promoter or open reading frame (ORF) region or (iii) a pair of nucleotide and G1962A representing specific double point mutations in the DNA precore/core promoter or ORF region. The method and kit is useful in precore/core promoter or ORF region. The method and kit is useful in sequence the long-term response of a host of HBV to 3TC therapy (also known as lamivudine). This sequence represents an oligonucleotide sequence used in the method of the invention to detect a mutation in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #159 to determine effect of long term lamivudine treatment of HBV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Predicting the long-term response of a host of hepatitis B virus (HBV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ss; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine.
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   0; Indels
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 31; SEQ ID NO 159; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerin JL;
                                                                          1 AAATTCTTTATAAGGGUCGA
                                                                                                                                             25 AAATTCTTTATAAGGGTCGA
                                                                                                                                                                                                                                                                                                                                              ВÞ
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                                                                                                                                                                                                                                                                                                                                      ADN36078 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-348004/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004031729-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                ADN36078;
Matches
                                                                                                                                                                                                                                                                                                      ADN36078/
XXX ADN3
XXX ADN3
XXX ADN3
XXX B8;
XXX W020
XXX
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Predicting the long-term response of a host of hepatitis B virus (HBV) 3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.

Gerin JL;

(GEOU) UNIV GEORGETOWN Korba BE, Ciancio A, WPI; 2004-348004/32.

01-OCT-2003; 2003WO-US031121. 01-OCT-2002; 2002US-0415301P.

15-APR-2004

Claim 31; SEQ ID NO 158; 107pp; English

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The invention relates to a method of predicting the long term response of
a host of hepatitis B virus (HBV) to 3TC therapy by determining whether
the HBV carried by the host (i) bears a nucleic acid that encodes for a
leucine at amino acid position (aa) 91 in the DNA polymerase region
(originally codon 438) or a (ii) a cysteine at aa256 (originally codon
(originally codon 438) or a (ii) a cysteine at aa256 (originally codon
(originally codon 438) or a (ii) a cysteine at aa256 (originally codon
(originally codon 438) or a (ii) a cysteine at aa213) (originally
determining whether the HBV carried by the host bears one or more of the
following mutations: (i) Q2138 (glutamine to serine at aa213) (originally
codon 604) in the HBV polymerase region, (ii) G17397, A1732C/T, T1909C,
T1960G, or T1961A/G specific point mutation in the DNA precore/core
promoter or open reading frame (ORP) region or (iii) a pair of nucleotide
changes A138C and G1739T, A175CG and A1752G, T1909G and A1911T or T1961A

or and C1962A representing specific double point mutations in the DNA
precore/core promoter or ORF region. The method and kit is useful in
predicting the long-term response of a host of HBV to 3TC therapy (also
known as lamivudine). This sequence represents an oligonucleotide
chown as lamivudine). This sequence represents an oligonucleotide
conduction of the invention to detect a mutation in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 12; Length 28; 95.0%; Pred. No. 7.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28 BP; 10 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN36076 standard; DNA; 28 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          above mentioned sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-2004
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Gaps

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0; Indels

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Best Local Similarity

Query Match

1 AAATTCTTTATAAGGGUCGA 20

22 AAATTCTTTATAAGGGTCGA 3

RESULT 12 ADN36077/c

95.0%; Pred. No.

100.0%; Score 20; DB 12; Length 28; 95.0%; Pred. No. 7.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                   Predicting the long-term response of a host of hepatitis B virus (HBV) to 3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe #153 to determine effect of long term lamivudine treatment of HBV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88; probe; hepatitis B virus; HBV; 3TC therapy; mutation; lamivudine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 12; Length 28; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28 BP; 10 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                 Claim 31; SEQ ID NO 157; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAATTCTTTATAAGGGUCGA 20
                                                                                                                                                       Gerin JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 AAATTCTTTATAAGGGTCGA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
95.0%; F
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ADN36072 standard; DNA; 28 BP
                                                                                01-OCT-2003; 2003WO-US031121.
                                                                                                       01-OCT-2002; 2002US-0415301P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   above mentioned sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Conservative
                                                                                                                                (GEOU ) UNIV GEORGETOWN
                                                                                                                                                      Ciancio A,
                                                                                                                                                                              WPI; 2004-348004/32.
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Best Local Similarity
         Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus.
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                                                          15-APR-2004
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The invention relates to a method of predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy by determining whether the HBV carried by the host (i) bears a nucleic acid that encodes for a leucine at amino acid position (as) 91 in the DNA polymerase region (originally codon 438) or a (ii) a cysteine at aa256 (originally codon 604) in the DNA polymerase region of HBV. The method comprises cederamining whether the HBV carried by the host bears one or more of the following mutations: (i) 02133 (glutamine to serine at aa213) (originally codon 604) in the HBV polymerase region, (ii) 61739T, A1752C/T, T1909C, T1960G, or T1961A/G specific point mutation in the DNA precore/core promoter or open reading frame (ORF) region or (iii) a pair of nucleotide changes A1738C and G1739T, A1750G and A1752G, T1909G and A1911T or T1961A and C1962A representing specific double point mutations in the DNA compore or ORF region. The method and kit is useful in precore/core promoter or ORF region. The method and kit is useful in the method of the invention to detect a mutation in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #160 to determine effect of long term lamivudine treatment of HBV.
                                                                                                                                                                                                                                                Predicting the long-term response of a host of hepatitis B virus (HBV) 3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAATTCTTTATAAGGGUCGA 20
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                                                                                                                             Gerin JL;
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01-OCT-2002; 2002US-0415301P.
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                                                            (GEOU ) UNIV GEORGETOWN
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                                                                                                                             Korba BE,
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3TC therapy comprises determining whether the HBV bears a nucleic acid encoding leucine at amino acid position (aa) 91 or cysteine at aa256.

Claim 31; SEQ ID NO 160; 107pp; English.

The invention relates to a method of predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy by determining whether the HBV carried by the host (i) bears a nucleic acid that encodes for a leucine at amino acid position (as) 91 in the DNA polymerase region (criginally codon 438) or a (ii) a cysteine at aa256 (originally codon 604) in the DNA polymerase region of HBV. The method comprises determining whether the HBV carried by the host bears one or more of the collowing mutations: (i) Q2135 (glutamine to serine at aa213) (originally codon 604) in the HBV polymerase region, (ii) G1397, A1752CT, T1909C, T1960G, or T1961A/G specific point mutation in the DNA precore/core promoter or open reading frame (ORF) region or (iii) a pair of nucleotide changes A1738C and G1739T, A1750G and A1752G, T1909G and A1911T or T1961A and C1962A representing specific double point mutations in the DNA precore/core promoter or ORF region. The method and kit is useful in predicting the long-term response of a hose of HBV to 3TC therapy (also known as lamivudine). This sequence represents an oligonucleotide sequence used in the method of the invention to detect a mutation in the above mentioned sequences.

Sequence 28 BP; 9 A; 5 C; 5 G; 9 T; 0 U; 0 Other;

0; Gaps 100.0%; Score 20; DB 12; Length 28; 95.0%; Pred. No. 7.1; o; Indels tive 1; Mismatches 0; Indels Query Match
Best Local Similarity 95.0
Matches 19; Conservative

1 AAATTCTTTATAAGGGUCGA 20

g ò

Search completed: March 17, 2005, 06:48:45 Job time : 172.333 secs

us-08-901-612a-65.rst

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March 17, 2005, 05:44:58; Search time 1386.27 Seconds (without alignments) 549.162 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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20
1 aaattctttataagggucga 20
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9b htc: *
9b est3: *
9b est4: *
9b est6: *
9b 9s81: *
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| ion | ~ ~ | BES182410 T3 end of | T3 end of T7 end of | Š | AV258784 | | | _ | | Forward B | | rswgb0_00 | Ношо варі | Schmidtea | Homo sapi | Pan trogl | HO13B17w | PP LEA000 | tigr-gss- |
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| Description | CL798479 CA029935 | CK125419 AL397847 | AL401256 AL401255 | AG265169 | AV258784 | CA856765 | BI926889 | BP527047 | CE435953 | CR154100 CD865385 | CF424535 | CK537618 | AG016570 | AY068711 | AG016569 | AG119858 | CK569388 | BU041523 | CE761259 |
| 70 | | | | | | | | | | | | | | | | | | | |
| SUMMARIES | CL798479 CA029935 | CK125419 CNS06GLD | CNS06J82 CNS06J81 | AG265169 | AV258784 | CA856765 | BI926889 | BP527047 | CE435953 | CR154100 CD865385 | CF424535 | CK537618 | AG016570 | AY068711 | AG016569 | AG119858 | CK569388 | BU041523 | CE761259 |
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| % Query Match | 90.0 | 87.0 87.0 | 87.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 |
| Score | 18 | 17.4 | 17.4 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 |
| ult No. | н 7 | W 4 | ın v | ۲, | 0 00 | 10 | 11 | 12 | £ : | 14 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 |
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| AG597534 Mus muscu CL748062 OR BBA011 CC895730 CR68520 OR BBA011 472 CL620368 OR BBA001 472 CL18472 ISB1-70N2 NTK CC240216 CR261-121 643 AL406422 T3 end of CC240216 CR261-121 BH783463 fambol186 207 CL612841 OR BBA005 CL72841 OR BBA006 CL72841 OR BBA006 CL72841 OR BBA006 CL78251 OR BBA006 A1556720 UI-R-C2p- CL611235 OR BBA006 A1556720 UI-R-C2p- CL611235 OR BBA006 CL730394 OR BBA006 BU2671162 BW030883 BW030883 BW030883 BW310881765 BW030883 BW030883 A17065 BJ66669 BJ666669 BB646609 | MENTS bp DNA | Lipogon genomic cione or tophyta; Embryophyta; Tra | ., Yost,D., Stum,D., Rao,K., Luo,M., r,C., Hatfield,J., Soderlund,C. and | ity of Arizona 8 | |
|--|---------------------------------|--|--|--|---|
| AGS97534 CL748062 CC895730 CC895730 CC805730 CL620368 CC18472 CC806N7K CC40216 B CC40216 B CC4034207 CL728817 CL728817 CL728817 CL728817 CL73034 A BU267130 CL551502 B BW030186 B B | | 1 OK LEG OLYZG rvey sequence.:51021406 n nidiplantae; St Magnoliophyta Oryzeae; Oryzeae; Oryzeae; | sotski, M ., Mulle 19 19 | ona 303, ne.arizo AC TCA C TTA GGC C GAC TC Dualifie "Cason: 4 "Cason: 4 "Cason: 4 "Cason: 4 "Cason: 6 "Cason: | |
| 750 942 943 943 110 1113 113 312 312 312 312 312 312 312 31 | | : survey GI:5102 Ogon Viridipl 'ta; Magr | ss 1 to 866) Yu,Y., Wissotski, , Kudrna,D., Mull, ject nded (2004) Rod A. Wing Genomics Institut | y of Arizona ilding Room 303, Tucson, 626 9595 621 1259 tp://genome.arizona.edu TAA TAC GAC TCA CTA TAG (GAC TCA TTA GGC ACC CCA O9 row. F column: 12 Tr. TAA TAC GAC TCA CTA TAG (C ends. Location/Qualifiers 1. 866 /organism="Coryza rufipoga" /mol type="genomic DNA" /db_xref="taxon:4529" /tlssue_type="young leav, /dev_stage="young leav, /d | *************************************** |
| ###################################### | 798479 | or Caronoverial Or Lea Olyza in Caronoverial Curjo8479 CL/98479.1 G1:51021406 GSS. Oryza rufipogon Oryza rufipogon Oryza rufipogon Sukaryota; Viridiplantae; Strep Spermatophyta; Magnoliophyta; L Ehrhartoideae; Oryzaeae; Oryza. | 1 (bases 1 t Kim, H., Yu, Y., Jetty, R., Kud Wing, R. OMAP project Unpublished Contact: Rod Arizona Genom | University of Arizona Forbes Building Room 303, Tucson Fax: 520 621 1259 Email: http://genome.arizona.edu Epre PRimers FORMARD: TAA TAC GAC TCA TAG BACKWARD: TAA TAC GAC TCA CC BACKWARD: TAA TAC GAC TCA TAG BACKWARD: TAA TAC GAC TCA TAG BACKWARD: TAA TAC GAC TCA TAG Class: BAC ends. Location/Qualifiers Location/Gualifiers Location/Appe="genomic DNA" Adb_xref="taxon:4529" Clone="Note:"Public TI phan Clone="Vector: pAGIBACI Adv treated 36 hrs befo | |
| $\begin{array}{c} 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 $ | GL7 | - - | | O | ÷ |
| 0 0 00000 | RESULT 1 CL798479/c LOCUS | ACCESSION VERSION VERYORDS SOURCE ORGANISM | REFERENCE AUTHORS TITLE JOURNAL COMMENT | FEATURES SOUIC | ORIGIN Metch |

94.48;

Best Local Similarity 94.4 Matches 17; Conservative

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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Bukaryorts, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Bukaryorts, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticeae; Hordeum.

SE Kramer, A.; Feilner, T.; Possling, A.; Radchuk, V.; Weschke, W.;

Buerkle, L. and Kersten, B.

Application of the protein microarray technology for the identification of expression library derived target proteins for barley protein kinase CK2

Mupublished (2003)

Contact: Birgit Kersten* and Winfriede Weschke**

*Plant Protein Chip Group, Department Lehrach, **Department Molecular Genetics, Gene Expression Group

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Gatersleben, Germany, **Corrensstrasse 3, D-06466

Tel: *+49(0)30/84131128,**+49(0)394825500

Fax: *+49(0)30/84131128,**+49(0)394825537

Email: *kerstensmolgen.mpg.de, **Weschke@ipk-gatersleben.de

Insert Length: 893 Std Brror: 0.00

Plate: 7 row, P. column: 7
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/db xref="fdAB1:94977"
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/dev stage="embryosac"
/dev st
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Hordeum vulgare subsp. vulgare"
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                                    CK125419.1 GI:44808421
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                                                                                                                                                                                                                                                                                                                                  HX05J231 HX Hordeum vulgare subsp. vulgare cDNA clone HX05J23
5-PRIME, mRNA sequence.
CA029935 GA29935.1 GI:24325281
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Hordeum vulgare subsp. vulgare
Bukaryota, Viridibantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 624)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Contact: Stein Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 01-MAR-2004
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/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PetI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              693 bp mRNA linear EST 01-MAR-2
BES1824107p07 BES1824 Hordeum vulgare subsp. vulgare cDNA clone
MPMGp2010P077 5-PRIME, mRNA sequence.
CK125419
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Institute of Plant Genetics and Crop Plant Research (IPK)
Correnser. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
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89.5%; Pred. No. 8.5e+02;
.ive 1; Mismatches 1; Indels (
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Pred, No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sub_species="vulgare"
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/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: stein@ipk-gatersleben.de
Insert Length: 624 Std Brror: 0.00
Plate: 5 row: J column: 23
Seg primer: Ml3rev.
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Fax: 039482-5595

source

FEATURES

SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

RESULT 2 CA029935/c

셤

DEFINITION

ACCESSION VERSION KEYWORDS 17; Conservative

RESULT 3 CK125419/c

g

LOCUS

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Query Match Best Local Similarity Matches 17; Conservat

DRIGIN

ORGANISM

REFERENCE

JOURNAL MEDLINE

TITLE

PUBMED REFERENCE

JOURNAL PUBMED REFERENCE AUTHORS

TITLE

AUTHORS TITLE JOURNAL

COMMENT

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Genoscope.

Direct Submission

Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

8 eqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
               Sm. Saccharomyces bayanus
Saccharomyces bayanus
Saccharomyces bayanus
Bukaryota; Rungi; Ascomycota; Saccharomycetials;
Saccharomycetales; Saccharomycetaceae; Saccharomycets.

E (bases 1 to 103)
Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Gelotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Malpertuy, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Sautin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
20594711

E 20594711
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Trend of clone ASOAA026F08 of library ASOAA from strain CLIB 533
AL401255
AL401255.1 GI:12158665
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//note="similar to Saccharomyces cerevisiae ORF YHR172w [
SPC97 ; spindle pole body component ]
1 putative frameshift(s)"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bon, E., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P., Aigle, M. and Durrens, P. Benomic exploration of the hemiascomycetous yeasts: 5. Saccharomyces bayanus var. uvarum PEBS Lett. 487 (1), 37-41 (2000)
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89.5%; Pred. No. 8.9e+02;
ive 1; Mismatches 1; Indels 0;
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/organism="Saccharomyces bayanus"
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/strain="CLIB 533"
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   Saccharomyces bayanus
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Matches 17; Conservative
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AUTHORS
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqreféganoscope.cns.fr. - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

Incation/Qualifiers
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/note="similar to Saccharomyces cerevisiae ORF YHR172w [
SPC97.; spindle pole body component ]"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bon, B., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P., Aigle, M. and Durrens, P. Genomic exploration of the hemiascomycetous yeasts: 5.
                                                                                                                                  Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, B., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lephingle, A., Liorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Porier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                  Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces bayanus var. uvarum
PEBS Lett. 487 (1), 37-41 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4931"
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GSS.
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FEATURES

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Gaps

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DEFINITION

RESULT 5 CNS06J82

DRIGIN

ACCESSION

VERSION KEYWORDS

KEYWORDS SOURCE ORGANISM

AUTHORS REFERENCE

MEDLINE PUBMED

REFERENCE AUTHORS

JOURNAL

TITLE

MEDLINE PUBMED

REFERENCE

JOURNAL

TITLE

AUTHORS TITLE JOURNAL

COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E. (Dasses 1 to 293)
S. Komno, H., Adzawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Izawa, M., Kadota, K., Kagawa, I., Kadi, C., Kawai, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Ragawa, I., Kadi, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Salto, H., Satai, C., Sato, K.,
Shibata, Y., Shibata, Y., Shucki, H., Saukai, H., Taqawa, A.,
Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Taqawa, A.,
Fakahashi, F., Tominaqa, N., Toya, T., Tsunoda, Y., Watahiki, A.,
Watanabe, S., Yamamura, T., Yamanaka, I., Yasunishi, A.,
Hayashizaki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB009906 BIKEN full-length enriched, 10 day neonate skin Mus museculus cDNA clone 4732491N16 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research, 2-6-7
Kazusa-kamatari, Kisarau, Chiba 292-0818, Japan
(E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
Tel:81-438-52-3935(ex.2336), Pax:81-438-52-3934)
                                                       Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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The Institute of Physical and Chemical Research (RIKEN)
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/clone="t_jT62e07_sfi"
/clone_lib="genomic TAC library"
/note="VBCTOR:pVLTAC7~synonym: Lotus japonicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Lotus corniculatus var. japonicus"
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85.0%; Pred. No. 1.4e+03;
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Unpublished (2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                   Sato, S., Nakamura, Y. and Tabata, S. Cictus japonicus TAC End sequences Published Only in Database (2002) (bases 1 to 85)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /variety="japonicus"
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      AG265169.1 GI:26665008
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BB009906.1 GI:8130263
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Best Local Similarity
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BB009906/c
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 BYRY cedex, FRANCE. (E-mail:
8 gatson Cremieux, CP 5706, 91057 BYRY cedex, FRANCE. (E-mail:
8 agref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces Rluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1028)
Bon, E., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P.,
Aigle, M. and Durrens, P.
                                                                                                                                             1 (bases 1 to 1028)
Souciet, J.L., Aggle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
FEBS Lett. 487 (1), 3-12 (2000)
                                                 Saccharomyces bayanus
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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FEBS Lett. 487 (1), 37-41 (2000)
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2 putative frameshift(s)"
/evidence=not_experimental
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                                                                                                                                          (bases 1 to 1028)
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Source

FEATURES

RESULT 7 AG265169/c DEFINITION

ACCESSION

Matches

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Gaps

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Indels Length

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 299)

Scono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Eukunishi, Y., Hara, A., Hayateu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nokamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sado, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watenabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Yokota, T., Yoshide Hayashizaki

Inpublished (1999)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

H. 7-22 Suchiro-otho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="RIKEN full-length enriched, adult male testis (DH10B)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .299
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                                                                               Email: genome-reseasc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoattivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomatu,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
          Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31). cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLCI.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev stage="10 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 10 day neonate
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1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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1. .293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="4732491N16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="skin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="C57BL/6J"
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AV258784.1 GI:6246243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="mixed"
                                      Tel: 81-45-503-9222
Fax: 81-45-503-9216
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was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI." ö Gaps 0 84.0%; Score 16.8; DB 1; Length 299; 85.0%; Pred. No. 1.6e+03; Indels 1; Mismatches

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RESULT 10

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CA856765

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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BP527047
BP527047 MAT001 Nicotiana tabacum cDNA clone BY11812, mRNA
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1 (Dases 1 to 494)
Matsuoka,K., Tashiro,G., Horiguchi,T., Demura,T. and Fukuda,H. Profiling growth-phase dependent gene expression of tobacco BY-2 cells by comprehensive microarray analysis
Umpublished (2003)
Contact: Ken Matsuoka
                                                                                                                           Lycopersicon esculentum
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 462)
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, 0-3 mm buds (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="flower"
/dev_stage="0-3mm buds"
/dev_stage="0-3mm buds"
/dov_stage="0-3mm buds"
/dov_stage="0-3mm buds"
/dov_stage="0-6"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morphogenesis Research Group
RIKEN Plant Science Center
17-2 Subhirocho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9575
Fax: 81-45-503-9573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 84.0%; Score 16.8; DB 4; Length 462; Best Local Similarity 85.0%; Pred. No. 1.6e+03; Matches 17; Conservative 1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Lycopersicon esculentum"
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Clemson University
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                                                                                                     Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOA31E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T3.
Location/Qualifiers
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B1926889.1 GI:16235836
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BP527047.1 GI:52830774
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Contact: CUGI
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                                                                                                                                                                                 CA856765 407 bp mRNA linear EST 17-DEC-2002 PfESToac41h07.yl Plasmodium falciparum 3D7 gametocyte cDNA library Plasmodium falciparum 3D7 cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 407)
Tang K., Cole, K., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D., Marra, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I., Magaire, L., Richey, J., Wadkins, J., Kennedy, S., Levinso, D., Waterston, R., Wilson, R. and Sibley, D.
Wash U Plasmodium SST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Library was constructed by R. Haywood. DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco.
Location/Qualifiers
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ESTS46778 tomato flower, buds 0-3 mm Lycopersicon esculentum CDNA
clone cTOA31E1 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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/db_xref="taxon:36329"
/db_stage="gametocyte (stage III-V)"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="Plasmodium falciparum 3D7 gametocyte cDNA
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Contact: L. David Sibley
WashU Pleamodium EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1800
Fax: 314 286 1810
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1 AAATTCTTTATAAGGGUCGA 20
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Best Local Similarity 85.0
Matches 17; Conservative
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CD865385
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Email: by2@psc.riken.go.jp, URL:http://mrg.psc.riken.go.jp/strc/ht.bc.DNA library was constructed from mRNA isolated from lag (9 h), 10 and stationary (7 days) old BY-2 cells. Seq primer: M13 forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 27-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kirkness EF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (dog)
Canis familiaris
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 508)
1 (karkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE435953
tigr-gss-dog-17000335866781 Dog Library Canis familiaris genomic,
CR435cs.
                                                                                                                                                                                        /cell line="BY-2"
/clone lib="MAT001"
/note="Vector: pGEM-T easy; primer: M13 forward; mRNA
obtained from lag, log and stationary phase cells"
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/db xref="texxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BetXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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84.0%; Score 16.8; DB 5; Length 494;
Best Local Similarity 85.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 1; Mismatches 2; Indels C
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                                                                                1. .494
/organism="Nicotiana tabacum"
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/db xref="taxon:4097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .508
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                                                                     Location/Qualifiers
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Best Local Similarity
Matches 17; Conserv
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CALD'ALUU S72 bp DNA linear GSS 06-JUL-2004 FOrward strand read from insert in 3'HFRT insertion targeting and chromosome engineering clone MHPP347b24, genomic survey sequence. CRL54100. TGI:49932945 GSS; genome survey sequence; MUS musculus (house mouse) Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 572) Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J.J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A. Davies, M. Bigs, D. Davies, D. Davies
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Poprmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 588)
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Flax: His sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Contact: Genoplante
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85.0%; Pred. No. 1.7e+03;
iive 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .572
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
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/clone_lib="AZO2"
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us-08-901-612a-65.rst

Query Match
84.0%; Score 16.8; DB 6; Length 588;
Best Local Similarity 85.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0

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Search completed: March 17, 2005, 11:07:55 Job time : 1389.27 secs